



1241.22

SEQUENCE LISTING

<110> KYOWA HAKKO KOGYO CO., LTD.

<120> Shear Stress-Responsive Genes

<130> 1241.22

<140> US/10/089,320

<141> 2002-03-28

<150> JP 1999-280976

<151> 1999-10-01

<160> 181

<170> PatentIn Ver. 2.0

<210> 1

<211> 3817

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (440)..(1930)

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Met Asn Gly Pro Glu Asp Leu Pro Lys Ser Tyr

1

5

10

gac tat gac ctt atc atc att gga ggt ggc tca gga ggt ctg gca gct 520

Asp Tyr Asp Leu Ile Ile Ile Gly Gly Gly Ser Gly Gly Leu Ala Ala

15

20

25

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30 35 40	
gtc act ccc acc cct ctt gga act aga tgg ggt ctt gga gga aca tgt	616
Val Thr Pro Thr Pro Leu Gly Thr Arg Trp Gly Leu Gly Gly Thr Cys	
45 50 55	
gtg aat gtg ggt tgc ata cct aaa aaa ctg atg cat caa gca gct ttg	664
Val Asn Val Gly Cys Ile Pro Lys Lys Leu Met His Gln Ala Ala Leu	
60 65 70 75	
tta gga caa gcc ctg caa gac tct cga aat tat gga tgg aaa gtc gag	712
Leu Gly Gln Ala Leu Gln Asp Ser Arg Asn Tyr Gly Trp Lys Val Glu	
80 85 90	
gag aca gtt aag cat gat tgg gac aga atg ata gaa gct gta cag aat	760
Glu Thr Val Lys His Asp Trp Asp Arg Met Ile Glu Ala Val Gln Asn	
95 100 105	
cac att ggc tct ttg aat tgg ggc tac cga gta gct ctg cgg gag aaa	808
His Ile Gly Ser Leu Asn Trp Gly Tyr Arg Val Ala Leu Arg Glu Lys	
110 115 120	
aaa gtc gtc tat gag aat gct tat ggg caa ttt att ggt cct cac agg	856
Lys Val Val Tyr Glu Asn Ala Tyr Gly Gln Phe Ile Gly Pro His Arg	
125 130 135	
att aag gca aca aat aat aaa ggc aaa gaa aaa att tat tca gca gag	904
Ile Lys Ala Thr Asn Asn Lys Gly Lys Glu Lys Ile Tyr Ser Ala Glu	
140 145 150 155	
agt ttt ctc att gcc act ggt gaa aga cca cgt tac ttg ggc atc cct	952
Ser Phe Leu Ile Ala Thr Gly Glu Arg Pro Arg Tyr Leu Gly Ile Pro	
160 165 170	
ggc gac aaa gaa tac tgc atc agc agt gat gat ctt ttc tcc ttg cct	1000
Gly Asp Lys Glu Tyr Cys Ile Ser Ser Asp Asp Leu Phe Ser Leu Pro	
175 180 185	
tac tgc ccg ggt aag acc ctg gtt gtt gga gca tcc tat gtc gct ttg	1048
Tyr Cys Pro Gly Lys Thr Leu Val Val Gly Ala Ser Tyr Val Ala Leu	

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190	195	200	
gag tgc gct gga ttt ctt gct ggt att ggt tta ggc gtc act gtt atg			1096
Glu Cys Ala Gly Phe Leu Ala Gly Ile Gly Leu Gly Val Thr Val Met			
205	210	215	
gtt agg tcc att ctt ctt aga gga ttt gac cag gac atg gcc aac aaa			1144
Val Arg Ser Ile Leu Leu Arg Gly Phe Asp Gln Asp Met Ala Asn Lys			
220	225	230	235
att ggt gaa cac atg gaa gaa cat ggc atc aag ttt ata aga cag ttc			1192
Ile Gly Glu His Met Glu Glu His Gly Ile Lys Phe Ile Arg Gln Phe			
240	245	250	
gta cca att aaa gtt gaa caa att gaa gca ggg aca cca ggc cga ctc			1240
Val Pro Ile Lys Val Glu Gln Ile Glu Ala Gly Thr Pro Gly Arg Leu			
255	260	265	
aga gta gta gct cag tcc acc aat agt gag gaa atc att gaa gga gaa			1288
Arg Val Val Ala Gln Ser Thr Asn Ser Glu Glu Ile Ile Glu Gly Glu			
270	275	280	
tat aat acg gtg atg ctg gca ata gga aga gat gct tgc aca aga aaa			1336
Tyr Asn Thr Val Met Leu Ala Ile Gly Arg Asp Ala Cys Thr Arg Lys			
285	290	295	
att ggc tta gaa acc gta ggg gtg aag ata aat gaa aag act gga aaa			1384
Ile Gly Leu Glu Thr Val Gly Val Lys Ile Asn Glu Lys Thr Gly Lys			
300	305	310	315
ata cct gtc aca gat gaa gaa cag acc aat gtg cct tac atc tat gcc			1432
Ile Pro Val Thr Asp Glu Glu Gln Thr Asn Val Pro Tyr Ile Tyr Ala			
320	325	330	
att ggc gat ata ttg gag gat aag gtg gag ctc acc cca gtt gca atc			1480
Ile Gly Asp Ile Leu Glu Asp Lys Val Glu Leu Thr Pro Val Ala Ile			
335	340	345	
cag gca gga aga ttg ctg gct cag agg ctc tat gca ggt tcc act gtc			1528
Gln Ala Gly Arg Leu Leu Ala Gln Arg Leu Tyr Ala Gly Ser Thr Val			
350	355	360	

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 Lys Cys Asp Tyr Glu Asn Val Pro Thr Thr Val Phe Thr Pro Leu Glu
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tat ggt gct tgt ggc ctt tct gag gag aaa gct gtg gag aag ttt ggg 1624
 Tyr Gly Ala Cys Gly Leu Ser Glu Glu Lys Ala Val Glu Lys Phe Gly
 380 385 390 395

gaa gaa aat att gag gtt tac cat agt tac ttt tgg cca ttg gaa tgg 1672
 Glu Glu Asn Ile Glu Val Tyr His Ser Tyr Phe Trp Pro Leu Glu Trp
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acg att ccg tca aga gat aac aac aaa tgt tat gca aaa ata atc tgt 1720
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 415 420 425

aat act aaa gac aat gaa cgt gtt gtg ggc ttt cac gta ctg ggt cca 1768
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 Asn Ala Gly Glu Val Thr Gln Gly Phe Ala Ala Ala Leu Lys Cys Gly
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ctg acc aaa aag cag ctg gac agc aca att gga atc cac cct gtc tgt 1864
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gca gag gta ttc aca aca ttg tct gtg acc aag cgc tct ggg gca agc 1912
 Ala Glu Val Phe Thr Thr Leu Ser Val Thr Lys Arg Ser Gly Ala Ser
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 Ile Leu Gln Ala Gly Cys
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<211> 497

<212> PRT

<213> Homo sapiens

<400> 2

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Gln Tyr Gly Lys Lys Val Met Val Leu Asp Phe Val Thr Pro Thr Pro
35 40 45
Leu Gly Thr Arg Trp Gly Leu Gly Gly Thr Cys Val Asn Val Gly Cys
50 55 60
Ile Pro Lys Lys Leu Met His Gln Ala Ala Leu Leu Gly Gln Ala Leu
65 70 75 80
Gln Asp Ser Arg Asn Tyr Gly Trp Lys Val Glu Glu Thr Val Lys His
85 90 95
Asp Trp Asp Arg Met Ile Glu Ala Val Gln Asn His Ile Gly Ser Leu
100 105 110
Asn Trp Gly Tyr Arg Val Ala Leu Arg Glu Lys Lys Val Val Tyr Glu
115 120 125
Asn Ala Tyr Gly Gln Phe Ile Gly Pro His Arg Ile Lys Ala Thr Asn
130 135 140
Asn Lys Gly Lys Glu Lys Ile Tyr Ser Ala Glu Ser Phe Leu Ile Ala
145 150 155 160
Thr Gly Glu Arg Pro Arg Tyr Leu Gly Ile Pro Gly Asp Lys Glu Tyr
165 170 175
Cys Ile Ser Ser Asp Asp Leu Phe Ser Leu Pro Tyr Cys Pro Gly Lys
180 185 190
Thr Leu Val Val Gly Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe
195 200 205
Leu Ala Gly Ile Gly Leu Gly Val Thr Val Met Val Arg Ser Ile Leu
210 215 220
Leu Arg Gly Phe Asp Gln Asp Met Ala Asn Lys Ile Gly Glu His Met
225 230 235 240
Glu Glu His Gly Ile Lys Phe Ile Arg Gln Phe Val Pro Ile Lys Val

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245	250	255
Glu Gln Ile Glu Ala Gly Thr Pro Gly Arg Leu Arg Val Val Ala Gln		
260	265	270
Ser Thr Asn Ser Glu Glu Ile Ile Glu Gly Glu Tyr Asn Thr Val Met		
275	280	285
Leu Ala Ile Gly Arg Asp Ala Cys Thr Arg Lys Ile Gly Leu Glu Thr		
290	295	300
Val Gly Val Lys Ile Asn Glu Lys Thr Gly Lys Ile Pro Val Thr Asp		
305	310	315
Glu Glu Gln Thr Asn Val Pro Tyr Ile Tyr Ala Ile Gly Asp Ile Leu		
325	330	335
Glu Asp Lys Val Glu Leu Thr Pro Val Ala Ile Gln Ala Gly Arg Leu		
340	345	350
Leu Ala Gln Arg Leu Tyr Ala Gly Ser Thr Val Lys Cys Asp Tyr Glu		
355	360	365
Asn Val Pro Thr Thr Val Phe Thr Pro Leu Glu Tyr Gly Ala Cys Gly		
370	375	380
Leu Ser Glu Glu Lys Ala Val Glu Lys Phe Gly Glu Glu Asn Ile Glu		
385	390	395
Val Tyr His Ser Tyr Phe Trp Pro Leu Glu Trp Thr Ile Pro Ser Arg		
405	410	415
Asp Asn Asn Lys Cys Tyr Ala Lys Ile Ile Cys Asn Thr Lys Asp Asn		
420	425	430
Glu Arg Val Val Gly Phe His Val Leu Gly Pro Asn Ala Gly Glu Val		
435	440	445
Thr Gln Gly Phe Ala Ala Ala Leu Lys Cys Gly Leu Thr Lys Lys Gln		
450	455	460
Leu Asp Ser Thr Ile Gly Ile His Pro Val Cys Ala Glu Val Phe Thr		
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Trp Pro Arg Pro Pro Ala Pro Gly Pro Pro Pro Pro Pro Leu Pro Leu
          20             25             30
ctg ctc ctg ctc ctg gcc ggg ctg ctg ggc ggc gcg ggc gcg cag tac 146
Leu Leu Leu Leu Leu Ala Gly Leu Leu Gly Gly Ala Gly Ala Gln Tyr
          35             40             45
tcc agc gac cgg tgc agc tgg aag ggg agc ggg ctg acg cac gag gca 194
Ser Ser Asp Arg Cys Ser Trp Lys Gly Ser Gly Leu Thr His Glu Ala
          50             55             60
cac agg aag gag gtg gag cag gtg tat ctg cgc tgt gcg gcg ggt gcc 242
His Arg Lys Glu Val Glu Gln Val Tyr Leu Arg Cys Ala Ala Gly Ala
          65             70             75
gtg gag tgg atg tac cca aca ggt gct ctc atc gtt aac ctg cgg ccc 290
Val Glu Trp Met Tyr Pro Thr Gly Ala Leu Ile Val Asn Leu Arg Pro
          80             85             90             95
aac acc ttc tcg cct gcc cgg cac ctg acc gtg tgc atc agg tcc ttc 338
Asn Thr Phe Ser Pro Ala Arg His Leu Thr Val Cys Ile Arg Ser Phe
          100            105            110
acg gac tcc tcg ggg gcc aat att tat ttg gaa aaa act gga gaa ctg 386
Thr Asp Ser Ser Gly Ala Asn Ile Tyr Leu Glu Lys Thr Gly Glu Leu
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aga ctg ctg gta ccg gac ggg gac ggc agg ccc ggc cgg gtg cag tgt	434		
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130	135	140	
ttt ggc ctg gag cag ggc ggc ctg ttc gtg gag gcc acg ccg cag cag	482		
Phe Gly Leu Glu Gln Gly Gly Leu Phe Val Glu Ala Thr Pro Gln Gln			
145	150	155	
gat atc ggc cgg agg acc aca ggc ttc cag tac gag ctg gtt agg agg	530		
Asp Ile Gly Arg Arg Thr Thr Gly Phe Gln Tyr Glu Leu Val Arg Arg			
160	165	170	175
cac agg gcg tcg gac ctg cac gag ctg tct gcg ccg tgc cgt ccc tgc	578		
His Arg Ala Ser Asp Leu His Glu Leu Ser Ala Pro Cys Arg Pro Cys			
180	185	190	
agt gac acc gag gtg ctc cta gcc gtc tgc acc agc gac ttc gcc gtt	626		
Ser Asp Thr Glu Val Leu Leu Ala Val Cys Thr Ser Asp Phe Ala Val			
195	200	205	
cga ggc tcc atc cag caa gtt acc cac gag cct gag cgg cag gac tca	674		
Arg Gly Ser Ile Gln Gln Val Thr His Glu Pro Glu Arg Gln Asp Ser			
210	215	220	
gcc atc cac ctg cgc gtg agc aga ctc tat cgg cag aaa agc agg gtc	722		
Ala Ile His Leu Arg Val Ser Arg Leu Tyr Arg Gln Lys Ser Arg Val			
225	230	235	
ttc gag ccg gtg ccc gag ggt gac ggc cac tgg cag ggg cgc gtc agg	770		
Phe Glu Pro Val Pro Glu Gly Asp Gly His Trp Gln Gly Arg Val Arg			
240	245	250	255
acg ctg ctg gag tgt ggc gtg cgg ccg ggg cat ggc gac ttc ctc ttc	818		
Thr Leu Leu Glu Cys Gly Val Arg Pro Gly His Gly Asp Phe Leu Phe			
260	265	270	
act ggc cac atg cac ttc ggg gag gcg cgg ctc ggc tgt gcc cca cgc	866		
Thr Gly His Met His Phe Gly Glu Ala Arg Leu Gly Cys Ala Pro Arg			
275	280	285	

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Phe Lys Asp Phe Gln Arg Met Tyr Arg Asp Ala Gln Glu Arg Gly Leu
290 295 300

aac cct tgt gag gtt ggc acg gac tgactccgtg ggccgctgcc cttcctctcc 968
Asn Pro Cys Glu Val Gly Thr Asp
305 310

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<212> PRT

<213> Homo sapiens

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Leu Leu Leu Leu Ala Gly Leu Leu Gly Gly Ala Gly Ala Gln Tyr Ser
35 40 45

Ser Asp Arg Cys Ser Trp Lys Gly Ser Gly Leu Thr His Glu Ala His
50 55 60

Arg Lys Glu Val Glu Gln Val Tyr Leu Arg Cys Ala Ala Gly Ala Val
65 70 75 80

Glu Trp Met Tyr Pro Thr Gly Ala Leu Ile Val Asn Leu Arg Pro Asn

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85	90	95	
Thr Phe Ser Pro Ala Arg His Leu Thr Val Cys Ile Arg Ser Phe Thr			
100	105	110	
Asp Ser Ser Gly Ala Asn Ile Tyr Leu Glu Lys Thr Gly Glu Leu Arg			
115	120	125	
Leu Leu Val Pro Asp Gly Asp Gly Arg Pro Gly Arg Val Gln Cys Phe			
130	135	140	
Gly Leu Glu Gln Gly Gly Leu Phe Val Glu Ala Thr Pro Gln Gln Asp			
145	150	155	160
Ile Gly Arg Arg Thr Thr Gly Phe Gln Tyr Glu Leu Val Arg Arg His			
165	170	175	
Arg Ala Ser Asp Leu His Glu Leu Ser Ala Pro Cys Arg Pro Cys Ser			
180	185	190	
Asp Thr Glu Val Leu Leu Ala Val Cys Thr Ser Asp Phe Ala Val Arg			
195	200	205	
Gly Ser Ile Gln Gln Val Thr His Glu Pro Glu Arg Gln Asp Ser Ala			
210	215	220	
Ile His Leu Arg Val Ser Arg Leu Tyr Arg Gln Lys Ser Arg Val Phe			
225	230	235	240
Glu Pro Val Pro Glu Gly Asp Gly His Trp Gln Gly Arg Val Arg Thr			
245	250	255	
Leu Leu Glu Cys Gly Val Arg Pro Gly His Gly Asp Phe Leu Phe Thr			
260	265	270	
Gly His Met His Phe Gly Glu Ala Arg Leu Gly Cys Ala Pro Arg Phe			
275	280	285	
Lys Asp Phe Gln Arg Met Tyr Arg Asp Ala Gln Glu Arg Gly Leu Asn			
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Pro Cys Glu Val Gly Thr Asp			
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<212> DNA

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<221> CDS

<222> (49)..(2664)

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Gly Ala Ala Gln Glu Leu Gln Ala Lys Leu Ala Glu Ile Gly Ala Pro

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10

15

atc cag ggt aat cgc gag gag ctg gtg gag cgg ctg cag agc tac acc 153

Ile Gln Gly Asn Arg Glu Glu Leu Val Glu Arg Leu Gln Ser Tyr Thr

20

25

30

35

cgc cag act ggc atc gtg ctg aat cgg ccg gtt ttg aga ggg gaa gat 201

Arg Gln Thr Gly Ile Val Leu Asn Arg Pro Val Leu Arg Gly Glu Asp

40

45

50

ggg gac aaa gcc gct cca cct ccc atg tcg gca cag ctc cct gga att 249

Gly Asp Lys Ala Ala Pro Pro Pro Met Ser Ala Gln Leu Pro Gly Ile

55

60

65

ccc atg cca cca cca cct ttg gga ctc ccc cct ctg cag cct cct ccg 297

Pro Met Pro Pro Pro Pro Pro Leu Gly Leu Pro Pro Leu Gln Pro Pro Pro

70

75

80

cca ccc cca cca cct cca cca ggc ctt ggc ctt ggc ttt cct atg gcc 345

Pro Pro Pro Pro Pro Pro Pro Gly Leu Gly Leu Gly Phe Pro Met Ala

85

90

95

cac cca cca aat ttg ggg ccc ccg cct cct ctc cgt gtg ggt gag cca 393

His Pro Pro Asn Leu Gly Pro Pro Pro Pro Leu Arg Val Gly Glu Pro

100

105

110

115

gtg gca ctg tca gag gag gag cgg ctg aag ttg gct cag cag cag gcg 441

Val Ala Leu Ser Glu Glu Glu Arg Leu Lys Leu Ala Gln Gln Gln Ala

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135	140	145	
tcg ctg aag gaa cat gag ctc ttg gag cag cag aag cgg gca gct gtg			537
Ser Leu Lys Glu His Glu Leu Leu Glu Gln Gln Lys Arg Ala Ala Val			
150	155	160	
tta ctg gag cag gaa cga cag cag gag att gcc aag atg ggc acc cca			585
Leu Leu Glu Gln Glu Arg Gln Gln Glu Ile Ala Lys Met Gly Thr Pro			
165	170	175	
gtc cct cgg ccc cca caa gac atg ggc cag att ggt gtg cgc act cct			633
Val Pro Arg Pro Pro Gln Asp Met Gly Gln Ile Gly Val Arg Thr Pro			
180	185	190	195
ctg ggt cct cga gta gct gct cca gtg ggc cca gtg ggc ccc act cct			681
Leu Gly Pro Arg Val Ala Ala Pro Val Gly Pro Val Gly Pro Thr Pro			
200	205	210	
aca gtt ttg ccc atg gga gcc cct gtt ccc cgg cct cgt ggt ccc cca			729
Thr Val Leu Pro Met Gly Ala Pro Val Pro Arg Pro Arg Gly Pro Pro			
215	220	225	
ccg ccc cct gga gat gag aac aga gag atg gat gac ccc tct gtg ggc			777
Pro Pro Pro Gly Asp Glu Asn Arg Glu Met Asp Asp Pro Ser Val Gly			
230	235	240	
ccc aag atc ccc cag gct ttg gag aag atc ctg cag ctg aag gag agc			825
Pro Lys Ile Pro Gln Ala Leu Glu Lys Ile Leu Gln Leu Lys Glu Ser			
245	250	255	
cgc cag gaa gag atg aat tct cag cag gag gaa gag gaa atg gaa aca			873
Arg Gln Glu Glu Met Asn Ser Gln Gln Glu Glu Glu Glu Met Glu Thr			
260	265	270	275
gat gct cgc tcg tcc ctg ggc cag tca gcg tca gag act gag gag gac			921
Asp Ala Arg Ser Ser Leu Gly Gln Ser Ala Ser Glu Thr Glu Glu Asp			
280	285	290	

1241.22

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Thr Val Ser Val Ser Lys Lys Glu Lys Asn Arg Lys Arg Arg Asn Arg	
295 300 305	
aag aag aag aaa aag ccc cag cgg gtg cga ggg gtg tcc tct gag agc	1017
Lys Lys Lys Lys Lys Pro Gln Arg Val Arg Gly Val Ser Ser Glu Ser	
310 315 320	
tct ggg gac cgg gag aaa gac tca acc cgg tcc cgt ggc tct gat tcc	1065
Ser Gly Asp Arg Glu Lys Asp Ser Thr Arg Ser Arg Gly Ser Asp Ser	
325 330 335	
cca gca gct gat gtt gag att gag tat gtg act gaa gaa cct gaa att	1113
Pro Ala Ala Asp Val Glu Ile Glu Tyr Val Thr Glu Glu Pro Glu Ile	
340 345 350 355	
tac gag ccc aac ttt atc ttc ttt aag agg atc ttt gag gct ttt aag	1161
Tyr Glu Pro Asn Phe Ile Phe Phe Lys Arg Ile Phe Glu Ala Phe Lys	
360 365 370	
ctc act gat gat gtg aag aag gag aaa gag aaa gag cca gag aaa ctt	1209
Leu Thr Asp Asp Val Lys Lys Glu Lys Glu Lys Glu Pro Glu Lys Leu	
375 380 385	
gac aaa ctg gag aac tct gca gcc ccc aag aag aag gga ttt gaa gag	1257
Asp Lys Leu Glu Asn Ser Ala Ala Pro Lys Lys Lys Gly Phe Glu Glu	
390 395 400	
gag cac aag gac agt gat gat gac agc agt gat gac gag cag gaa aag	1305
Glu His Lys Asp Ser Asp Asp Asp Ser Ser Asp Asp Glu Gln Glu Lys	
405 410 415	
aag cca gaa gcc ccc aag ctg tcc aag aag aag ttg cgc cga atg aac	1353
Lys Pro Glu Ala Pro Lys Leu Ser Lys Lys Lys Leu Arg Arg Met Asn	
420 425 430 435	
cgc ttc act gtg gct gaa ctc aag cag ctg gtg gct cgg ccc gat gtc	1401
Arg Phe Thr Val Ala Glu Leu Lys Gln Leu Val Ala Arg Pro Asp Val	
440 445 450	
gtg gag atg cac gat gtg aca gcg cag gac cct aag ctc ttg gtt cac	1449
Val Glu Met His Asp Val Thr Ala Gln Asp Pro Lys Leu Leu Val His	

1241.22

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ctc aag gcc act cgg aac tct gtg cct gtg cca cgc cac tgg tgt ttt			1497
Leu Lys Ala Thr Arg Asn Ser Val Pro Val Pro Arg His Trp Cys Phe			
470	475	480	
aag cgc aaa tac ctg cag ggc aaa cgg ggc att gag aag ccc ccc ttc			1545
Lys Arg Lys Tyr Leu Gln Gly Lys Arg Gly Ile Glu Lys Pro Pro Phe			
485	490	495	
gag ctg cca gac ttc atc aaa cgc aca ggc atc cag gag atg cga gag			1593
Glu Leu Pro Asp Phe Ile Lys Arg Thr Gly Ile Gln Glu Met Arg Glu			
500	505	510	515
gcc ctg cag gag aag gaa gaa cag aag acc atg aag tca aaa atg cga			1641
Ala Leu Gln Glu Lys Glu Glu Gln Lys Thr Met Lys Ser Lys Met Arg			
520	525	530	
gag aaa gtt cgg cct aag atg ggc aaa att gac atc gac tac cag aaa			1689
Glu Lys Val Arg Pro Lys Met Gly Lys Ile Asp Ile Asp Tyr Gln Lys			
535	540	545	
ctg cat gat gcc ttc ttc aag tgg cag acc aag cca aag ctg acc atc			1737
Leu His Asp Ala Phe Phe Lys Trp Gln Thr Lys Pro Lys Leu Thr Ile			
550	555	560	
cat ggg gac ctg tac tat gag ggg aag gag ttc gag aca cga ctg aag			1785
His Gly Asp Leu Tyr Tyr Glu Gly Lys Glu Phe Glu Thr Arg Leu Lys			
565	570	575	
gag aag aag cca gga gat ctg tct gat gag cta agg att tcc ttg ggg			1833
Glu Lys Lys Pro Gly Asp Leu Ser Asp Glu Leu Arg Ile Ser Leu Gly			
580	585	590	595
atg cca gta gga cca aat gcc cac aag gtc cct ccc cca tgg ctg att			1881
Met Pro Val Gly Pro Asn Ala His Lys Val Pro Pro Pro Trp Leu Ile			
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gcc atg cag cga tat gga cca ccc cca tcg tat ccc aac ctg aaa atc			1929
Ala Met Gln Arg Tyr Gly Pro Pro Pro Ser Tyr Pro Asn Leu Lys Ile			
615	620	625	

1241.22

cct ggg ctg aac tcg ccc atc cct gag agc tgt tcc ttt ggg tac cat	1977
Pro Gly Leu Asn Ser Pro Ile Pro Glu Ser Cys Ser Phe Gly Tyr His	
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Ala Gly Gly Trp Gly Lys Pro Pro Val Asp Glu Thr Gly Lys Pro Leu	
645 650 655	
tat ggg gac gtg ttt gga acc aat gct gct gaa ttt cag acc aag act	2073
Tyr Gly Asp Val Phe Gly Thr Asn Ala Ala Glu Phe Gln Thr Lys Thr	
660 665 670 675	
gag gaa gaa gag att gat cgg acc cct tgg ggg gaa ctg gaa cca tct	2121
Glu Glu Glu Glu Ile Asp Arg Thr Pro Trp Gly Glu Leu Glu Pro Ser	
680 685 690	
gat gaa gaa tcc tca gaa gaa gag gaa gag gaa gaa agt gat gaa gac	2169
Asp Glu Glu Ser Ser Glu Glu Glu Glu Glu Glu Glu Ser Asp Glu Asp	
695 700 705	
aaa cca gat gag aca ggc ttt att acc cct gca gac agt ggc ctt atc	2217
Lys Pro Asp Glu Thr Gly Phe Ile Thr Pro Ala Asp Ser Gly Leu Ile	
710 715 720	
act cct gga ggc ttt tca tca gtg cct gct gga atg gag acc cct gaa	2265
Thr Pro Gly Gly Phe Ser Ser Val Pro Ala Gly Met Glu Thr Pro Glu	
725 730 735	
ctc att gag ctg agg aag aag aag att gag gag gcg atg gac gga agt	2313
Leu Ile Glu Leu Arg Lys Lys Lys Ile Glu Glu Ala Met Asp Gly Ser	
740 745 750 755	
gag aca cct cag ctc ttc act gtg ttg cca gag aag aga aca gcc act	2361
Glu Thr Pro Gln Leu Phe Thr Val Leu Pro Glu Lys Arg Thr Ala Thr	
760 765 770	
gtt gga ggg gcc atg atg gga tca acc cac att tat gac atg tcc acg	2409
Val Gly Gly Ala Met Met Gly Ser Thr His Ile Tyr Asp Met Ser Thr	
775 780 785	
gtt atg agc cgg aag ggc ccg gct cct gag ctg caa ggt gtg gaa gtg	2457
Val Met Ser Arg Lys Gly Pro Ala Pro Glu Leu Gln Gly Val Glu Val	

1241.22

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      805              810              815
aag tat gag gag cat gtg cgg gag cag cag gct caa gta gag aag gag 2553
Lys Tyr Glu Glu His Val Arg Glu Gln Gln Ala Gln Val Glu Lys Glu
      820              825              830              835
gac ttc agt gac atg gtg gct gag cac gct gcc aaa cag aag caa aaa 2601
Asp Phe Ser Asp Met Val Ala Glu His Ala Ala Lys Gln Lys Gln Lys
              840              845              850
aaa cgg aaa gct cag ccc cag gac agc cgt ggg ggc agc aag aaa tat 2649
Lys Arg Lys Ala Gln Pro Gln Asp Ser Arg Gly Gly Ser Lys Lys Tyr
              855              860              865
aag gag ttc aag ttt taggtcccct cacactagcc ctttttttgg ccctacgtct 2704
Lys Glu Phe Lys Phe
      870
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<212> PRT

<213> Homo sapiens

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              20              25              30
Ser Tyr Thr Arg Gln Thr Gly Ile Val Leu Asn Arg Pro Val Leu Arg
              35              40              45
Gly Glu Asp Gly Asp Lys Ala Ala Pro Pro Pro Met Ser Ala Gln Leu
              50              55              60
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1241.22

Pro Gly Ile Pro Met Pro Pro Pro Pro Leu Gly Leu Pro Pro Leu Gln
65 70 75 80
Pro Pro Pro Pro Pro Pro Pro Pro Pro Gly Leu Gly Leu Gly Phe
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Pro Met Ala His Pro Pro Asn Leu Gly Pro Pro Pro Pro Leu Arg Val
100 105 110
Gly Glu Pro Val Ala Leu Ser Glu Glu Glu Arg Leu Lys Leu Ala Gln
115 120 125
Gln Gln Ala Ala Leu Leu Met Gln Gln Glu Glu Arg Ala Lys Gln Gln
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Gly Asp His Ser Leu Lys Glu His Glu Leu Leu Glu Gln Gln Lys Arg
145 150 155 160
Ala Ala Val Leu Leu Glu Gln Glu Arg Gln Gln Glu Ile Ala Lys Met
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Gly Thr Pro Val Pro Arg Pro Pro Gln Asp Met Gly Gln Ile Gly Val
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Arg Thr Pro Leu Gly Pro Arg Val Ala Ala Pro Val Gly Pro Val Gly
195 200 205
Pro Thr Pro Thr Val Leu Pro Met Gly Ala Pro Val Pro Arg Pro Arg
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Gly Pro Pro Pro Pro Pro Gly Asp Glu Asn Arg Glu Met Asp Asp Pro
225 230 235 240
Ser Val Gly Pro Lys Ile Pro Gln Ala Leu Glu Lys Ile Leu Gln Leu
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Lys Glu Ser Arg Gln Glu Glu Met Asn Ser Gln Gln Glu Glu Glu Glu
260 265 270
Met Glu Thr Asp Ala Arg Ser Ser Leu Gly Gln Ser Ala Ser Glu Thr
275 280 285
Glu Glu Asp Thr Val Ser Val Ser Lys Lys Glu Lys Asn Arg Lys Arg
290 295 300
Arg Asn Arg Lys Lys Lys Lys Lys Pro Gln Arg Val Arg Gly Val Ser

1241.22
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 Ser Asp Ser Pro Ala Ala Asp Val Glu Ile Glu Tyr Val Thr Glu Glu
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 Pro Glu Ile Tyr Glu Pro Asn Phe Ile Phe Phe Lys Arg Ile Phe Glu
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 Ala Phe Lys Leu Thr Asp Asp Val Lys Lys Glu Lys Glu Lys Glu Pro
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 Glu Lys Leu Asp Lys Leu Glu Asn Ser Ala Ala Pro Lys Lys Lys Gly
 385 390 395 400
 Phe Glu Glu Glu His Lys Asp Ser Asp Asp Asp Ser Ser Asp Asp Glu
 405 410 415
 Gln Glu Lys Lys Pro Glu Ala Pro Lys Leu Ser Lys Lys Lys Leu Arg
 420 425 430
 Arg Met Asn Arg Phe Thr Val Ala Glu Leu Lys Gln Leu Val Ala Arg
 435 440 445
 Pro Asp Val Val Glu Met His Asp Val Thr Ala Gln Asp Pro Lys Leu
 450 455 460
 Leu Val His Leu Lys Ala Thr Arg Asn Ser Val Pro Val Pro Arg His
 465 470 475 480
 Trp Cys Phe Lys Arg Lys Tyr Leu Gln Gly Lys Arg Gly Ile Glu Lys
 485 490 495
 Pro Pro Phe Glu Leu Pro Asp Phe Ile Lys Arg Thr Gly Ile Gln Glu
 500 505 510
 Met Arg Glu Ala Leu Gln Glu Lys Glu Glu Gln Lys Thr Met Lys Ser
 515 520 525
 Lys Met Arg Glu Lys Val Arg Pro Lys Met Gly Lys Ile Asp Ile Asp
 530 535 540
 Tyr Gln Lys Leu His Asp Ala Phe Phe Lys Trp Gln Thr Lys Pro Lys
 545 550 555 560
 Leu Thr Ile His Gly Asp Leu Tyr Tyr Glu Gly Lys Glu Phe Glu Thr

1241.22

565	570	575
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580	585	590
Ser Leu Gly Met Pro Val Gly Pro Asn Ala His Lys Val Pro Pro Pro		
595	600	605
Trp Leu Ile Ala Met Gln Arg Tyr Gly Pro Pro Pro Ser Tyr Pro Asn		
610	615	620
Leu Lys Ile Pro Gly Leu Asn Ser Pro Ile Pro Glu Ser Cys Ser Phe		
625	630	635
Gly Tyr His Ala Gly Gly Trp Gly Lys Pro Pro Val Asp Glu Thr Gly		
645	650	655
Lys Pro Leu Tyr Gly Asp Val Phe Gly Thr Asn Ala Ala Glu Phe Gln		
660	665	670
Thr Lys Thr Glu Glu Glu Glu Ile Asp Arg Thr Pro Trp Gly Glu Leu		
675	680	685
Glu Pro Ser Asp Glu Glu Ser Ser Glu Glu Glu Glu Glu Glu Ser		
690	695	700
Asp Glu Asp Lys Pro Asp Glu Thr Gly Phe Ile Thr Pro Ala Asp Ser		
705	710	715
Gly Leu Ile Thr Pro Gly Gly Phe Ser Ser Val Pro Ala Gly Met Glu		
725	730	735
Thr Pro Glu Leu Ile Glu Leu Arg Lys Lys Lys Ile Glu Glu Ala Met		
740	745	750
Asp Gly Ser Glu Thr Pro Gln Leu Phe Thr Val Leu Pro Glu Lys Arg		
755	760	765
Thr Ala Thr Val Gly Gly Ala Met Met Gly Ser Thr His Ile Tyr Asp		
770	775	780
Met Ser Thr Val Met Ser Arg Lys Gly Pro Ala Pro Glu Leu Gln Gly		
785	790	795
Val Glu Val Ala Leu Ala Pro Glu Glu Leu Glu Leu Asp Pro Met Ala		
805	810	815

1241.22

Met Thr Gln Lys Tyr Glu Glu His Val Arg Glu Gln Gln Ala Gln Val
 820 825 830

Glu Lys Glu Asp Phe Ser Asp Met Val Ala Glu His Ala Ala Lys Gln
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<213> Homo sapiens

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 ctggtccccc gaggtctctg ccagtctgac agtgttcttg gcactgctca aaggtcccag 180
 cagctgggggt tccccgtcag cccgtgagcg gcc atg tcc aac ccc agc gcc cca 234

Met Ser Asn Pro Ser Ala Pro

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cca cca tat gaa gac cgc aac ccc ctg tac cca ggc cct ccg ccc cct 282
 Pro Pro Tyr Glu Asp Arg Asn Pro Leu Tyr Pro Gly Pro Pro Pro Pro

10

15

20

ggg ggc tat ggg cag cca tct gtc ctg cca gga ggg tat cct gcc tac 330
 Gly Gly Tyr Gly Gln Pro Ser Val Leu Pro Gly Gly Tyr Pro Ala Tyr

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35

cct ggc tac ccg cag cct ggc tac ggt cac cct gct ggc tac cca cag 378
 Pro Gly Tyr Pro Gln Pro Gly Tyr Gly His Pro Ala Gly Tyr Pro Gln

40

45

50

55

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Pro Met Pro Pro Thr His Pro Met Pro Met Asn Tyr Gly Pro Gly His																
60	65	70														
ggc tat gat ggg gag gag aga gcg gtg agt gat agc ttc ggg cct gga	474															
Gly Tyr Asp Gly Glu Glu Arg Ala Val Ser Asp Ser Phe Gly Pro Gly																
75	80	85														
gag tgg gat gac cgg aaa gtg cga cac act ttt atc cga aag gtt tac	522															
Glu Trp Asp Asp Arg Lys Val Arg His Thr Phe Ile Arg Lys Val Tyr																
90	95	100														
tcc atc atc tcc gtg cag ctg ctc atc act gtg gcc atc att gct atc	570															
Ser Ile Ile Ser Val Gln Leu Leu Ile Thr Val Ala Ile Ile Ala Ile																
105	110	115														
ttc acc ttt gtg gaa cct gtc agc gcc ttt gtg agg aga aat gtg gct	618															
Phe Thr Phe Val Glu Pro Val Ser Ala Phe Val Arg Arg Asn Val Ala																
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Val Tyr Tyr Val Ser Tyr Ala Val Phe Val Val Thr Tyr Leu Ile Leu																
140	145	150														
gcc tgc tgc cag gga ccc aga cgc cgt ttc cca tgg aac atc att ctg	714															
Ala Cys Cys Gln Gly Pro Arg Arg Arg Phe Pro Trp Asn Ile Ile Leu																
155	160	165														
ctg acc ctt ttt act ttt gcc atg ggc ttc atg acg ggc acc att tcc	762															
Leu Thr Leu Phe Thr Phe Ala Met Gly Phe Met Thr Gly Thr Ile Ser																
170	175	180														
agt atg tac caa acc aaa gcc gtc atc att gca atg atc atc act gcg	810															
Ser Met Tyr Gln Thr Lys Ala Val Ile Ile Ala Met Ile Ile Thr Ala																
185	190	195														
gtg gta tcc att tca gtc acc atc ttc tgc ttt cag acc aag gtg gac	858															
Val Val Ser Ile Ser Val Thr Ile Phe Cys Phe Gln Thr Lys Val Asp																
200	205	210	215													
ttc acc tcg tgc aca ggc ctc ttc tgt gtc ctg gga att gtg ctc ctg	906															
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1241.22

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Val Thr Gly Ile Val Thr Ser Ile Val Leu Tyr Phe Gln Tyr Val Tyr			
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tgg ctc cac atg ctc tat gct gct ctg ggg gcc att tgt ttc acc ctg			1002
Trp Leu His Met Leu Tyr Ala Ala Leu Gly Ala Ile Cys Phe Thr Leu			
250	255	260	
ttc ctg gct tac gac aca cag ctg gtc ctg ggg aac cgg aag cac acc			1050
Phe Leu Ala Tyr Asp Thr Gln Leu Val Leu Gly Asn Arg Lys His Thr			
265	270	275	
atc agc ccc gag gac tac atc act ggc gcc ctg cag att tac aca gac			1098
Ile Ser Pro Glu Asp Tyr Ile Thr Gly Ala Leu Gln Ile Tyr Thr Asp			
280	285	290	295
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Ile Ile Tyr Ile Phe Thr Phe Val Leu Gln Leu Met Gly Asp Arg Asn			
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1241.22

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<212> PRT

<213> Homo sapiens

<400> 8

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				20					25					30	
Pro	Gly	Gly	Tyr	Pro	Ala	Tyr	Pro	Gly	Tyr	Pro	Gln	Pro	Gly	Tyr	Gly
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His	Pro	Ala	Gly	Tyr	Pro	Gln	Pro	Met	Pro	Pro	Thr	His	Pro	Met	Pro
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Ser	Asp	Ser	Phe	Gly	Pro	Gly	Glu	Trp	Asp	Asp	Arg	Lys	Val	Arg	His
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Thr	Phe	Ile	Arg	Lys	Val	Tyr	Ser	Ile	Ile	Ser	Val	Gln	Leu	Leu	Ile
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				115					120					125	
Phe	Val	Arg	Arg	Asn	Val	Ala	Val	Tyr	Tyr	Val	Ser	Tyr	Ala	Val	Phe
				130					135					140	
Val	Val	Thr	Tyr	Leu	Ile	Leu	Ala	Cys	Cys	Gln	Gly	Pro	Arg	Arg	Arg

1241.22

Met Pro Glu Lys Arg Pro Phe Glu Arg

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Leu Pro Ala Asp Val Ser Pro Ile Asn Tyr Ser Leu Cys Leu Lys Pro

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gtg agg cag gcg act aat cag att gtg atg aat tgt gct gat att gat 256

Val Arg Gln Ala Thr Asn Gln Ile Val Met Asn Cys Ala Asp Ile Asp

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Ile Ile Thr Ala Ser Tyr Ala Pro Glu Gly Asp Glu Glu Ile His Ala

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Thr Gly Phe Asn Tyr Gln Asn Glu Asp Glu Lys Val Thr Leu Ser Phe

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80

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cct agt act ctg caa aca ggt acg gga acc tta aag ata gat ttt gtt 400

Pro Ser Thr Leu Gln Thr Gly Thr Gly Thr Leu Lys Ile Asp Phe Val

90

95

100

105

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Gly Glu Leu Asn Asp Lys Met Lys Gly Phe Tyr Arg Ser Lys Tyr Thr

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acc cct tct gga gag gtg cgc tat gct gct gta aca cag ttt gag gct 496

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125

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Thr Asp Ala Arg Arg Ala Phe Pro Cys Trp Asp Glu Pro Ala Ile Lys

140

145

150

gca act ttt gat atc tca ttg gtt gtt cct aaa gac aga gta gct tta 592

Ala Thr Phe Asp Ile Ser Leu Val Val Pro Lys Asp Arg Val Ala Leu

155

160

165

1241.22

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Leu Val Glu Val Lys Phe Ala Arg Thr Pro Val Met Ser Thr Tyr Leu	
190 195 200	
gtg gca ttt gtt gtg ggt gaa tat gac ttt gta gaa aca agg tca aaa	736
Val Ala Phe Val Val Gly Glu Tyr Asp Phe Val Glu Thr Arg Ser Lys	
205 210 215	
gat ggt gtg tgt gtc cgt gtt tac act cct gtt ggc aaa gca gag caa	784
Asp Gly Val Cys Val Arg Val Tyr Thr Pro Val Gly Lys Ala Glu Gln	
220 225 230	
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Gly Lys Phe Ala Leu Glu Val Ala Ala Lys Thr Leu Pro Phe Tyr Lys	
235 240 245	
gac tac ttc aat gtt cct tat cct cta cct aaa att gat ctc att gct	880
Asp Tyr Phe Asn Val Pro Tyr Pro Leu Pro Lys Ile Asp Leu Ile Ala	
250 255 260 265	
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Ile Ala Asp Phe Ala Ala Gly Ala Met Glu Asn Trp Gly Leu Val Thr	
270 275 280	
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Tyr Arg Glu Thr Ala Leu Leu Ile Asp Pro Lys Asn Ser Cys Ser Ser	
285 290 295	
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Ser Arg Gln Trp Val Ala Leu Val Val Gly His Glu Leu Ala His Gln	
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Trp Phe Gly Asn Leu Val Thr Met Glu Trp Trp Thr His Leu Trp Leu	
315 320 325	
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330					335					340					345				
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Phe	Pro	Glu	Tyr	Asp	Ile	Trp	Thr	Gln	Phe	Val	Ser	Ala	Asp	Tyr	Thr				
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cgt	gcc	cag	gag	ctt	gac	gcc	tta	gat	aac	agc	cat	cct	att	gaa	gtc	1216			
Arg	Ala	Gln	Glu	Leu	Asp	Ala	Leu	Asp	Asn	Ser	His	Pro	Ile	Glu	Val				
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agt	gtg	ggc	cat	cca	tct	gag	gtt	gat	gag	ata	ttt	gat	gct	ata	tca	1264			
Ser	Val	Gly	His	Pro	Ser	Glu	Val	Asp	Glu	Ile	Phe	Asp	Ala	Ile	Ser				
				380					385					390					
tat	agc	aaa	ggg	gca	tct	gtc	atc	cga	atg	ctg	cat	gac	tac	att	ggg	1312			
Tyr	Ser	Lys	Gly	Ala	Ser	Val	Ile	Arg	Met	Leu	His	Asp	Tyr	Ile	Gly				
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gat	aag	gac	ttt	aag	aaa	gga	atg	aac	atg	tat	tta	acc	aag	ttc	caa	1360			
Asp	Lys	Asp	Phe	Lys	Lys	Gly	Met	Asn	Met	Tyr	Leu	Thr	Lys	Phe	Gln				
410					415					420					425				
caa	aag	aat	gct	gcc	aca	gag	gat	ctc	tgg	gaa	agt	tta	gaa	aat	gct	1408			
Gln	Lys	Asn	Ala	Ala	Thr	Glu	Asp	Leu	Trp	Glu	Ser	Leu	Glu	Asn	Ala				
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Ser	Gly	Lys	Pro	Ile	Ala	Ala	Val	Met	Asn	Thr	Trp	Thr	Lys	Gln	Met				
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Leu	Leu	Arg	Leu	Ser	Gln	Lys	Lys	Phe	Cys	Ala	Gly	Gly	Ser	Tyr	Val				
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1241.22

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Glu Asp Pro Asn Gln Ala Lys Leu Lys Ile Leu Met Asp Lys Pro Glu	
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Met Asn Val Val Leu Lys Asn Val Lys Pro Asp Gln Trp Val Lys Leu	
525 530 535	
aac tta gga aca gtt ggg ttt tat cgg acc cag tac agc tct gcc atg	1744
Asn Leu Gly Thr Val Gly Phe Tyr Arg Thr Gln Tyr Ser Ser Ala Met	
540 545 550	
ctg gaa agt tta tta cca ggc att cgt gac ctt tct ctg ccc cct gtg	1792
Leu Glu Ser Leu Leu Pro Gly Ile Arg Asp Leu Ser Leu Pro Pro Val	
555 560 565	
gat cga ctt gga tta cag aat gac ctc ttc tcc ttg gct cga gct gga	1840
Asp Arg Leu Gly Leu Gln Asn Asp Leu Phe Ser Leu Ala Arg Ala Gly	
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atc att agc act gta gag gtt cta aaa gtc atg gag gct ttt gtg aat	1888
Ile Ile Ser Thr Val Glu Val Leu Lys Val Met Glu Ala Phe Val Asn	
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gag ccc aat tat act gta tgg agc gac ctg agc tgt aac ctg ggg att	1936
Glu Pro Asn Tyr Thr Val Trp Ser Asp Leu Ser Cys Asn Leu Gly Ile	
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ctc tca act ctc ttg tcc cac aca gac ttc tat gag gaa atc cag gag	1984
Leu Ser Thr Leu Leu Ser His Thr Asp Phe Tyr Glu Glu Ile Gln Glu	
620 625 630	
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Phe Val Lys Asp Val Phe Ser Pro Ile Gly Glu Arg Leu Gly Trp Asp	
635 640 645	
ccc aaa cct gga gaa ggt cat ctc gat gca ctc ctg agg ggc ttg gtt	2080
Pro Lys Pro Gly Glu Gly His Leu Asp Ala Leu Leu Arg Gly Leu Val	
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1241.22

Leu Gly Lys Leu Gly Lys Ala Gly His Lys Ala Thr Leu Glu Glu Ala	
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Arg Arg Arg Phe Lys Asp His Val Glu Gly Lys Gln Ile Leu Ser Ala	
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Asp Leu Arg Ser Pro Val Tyr Leu Thr Val Leu Lys His Gly Asp Gly	
700	705
act act tta gat att atg tta aaa ctt cat aaa caa gca gat atg caa	2272
Thr Thr Leu Asp Ile Met Leu Lys Leu His Lys Gln Ala Asp Met Gln	
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gaa gag aaa aac cga atc gaa aga gtc ctt ggc gct act ctt ttg cct	2320
Glu Glu Lys Asn Arg Ile Glu Arg Val Leu Gly Ala Thr Leu Leu Pro	
730	735
gac ctg att caa aaa gtc ctc acg ttt gca ctt tca gaa gag gta cgt	2368
Asp Leu Ile Gln Lys Val Leu Thr Phe Ala Leu Ser Glu Glu Val Arg	
750	755
cca cag gac act gta tcg gta att ggt gga gta gct gga ggc agc aag	2416
Pro Gln Asp Thr Val Ser Val Ile Gly Gly Val Ala Gly Gly Ser Lys	
765	770
cat ggt agg aaa gct gct tgg aaa ttc ata aag gac aac tgg gaa gaa	2464
His Gly Arg Lys Ala Ala Trp Lys Phe Ile Lys Asp Asn Trp Glu Glu	
780	785
ctt tat aac cga tac cag gga gga ttc tta ata tcc aga cta ata aag	2512
Leu Tyr Asn Arg Tyr Gln Gly Gly Phe Leu Ile Ser Arg Leu Ile Lys	
795	800
cta tca gtt gag gga ttt gca gtt gat aaa atg gct gga gag gtt aag	2560
Leu Ser Val Glu Gly Phe Ala Val Asp Lys Met Ala Gly Glu Val Lys	
810	815
gct ttc ttc gag agt cac cca gct cct tca gct gag cgt acc atc cag	2608
Ala Phe Phe Glu Ser His Pro Ala Pro Ser Ala Glu Arg Thr Ile Gln	
830	835
	840

1241.22

cag tgt tgt gaa aat att ctg ctg aat gct gcc tgg cta aag cga gat	2656
Gln Cys Cys Glu Asn Ile Leu Leu Asn Ala Ala Trp Leu Lys Arg Asp	
845 850 855	
gct gag agc atc cac cag tac ctc ctt cag cgg aag gcc tca cca ccc	2704
Ala Glu Ser Ile His Gln Tyr Leu Leu Gln Arg Lys Ala Ser Pro Pro	
860 865 870	
aca gtg tgaatcctga ggtgccgcc ttggcggttc tgctgcttcg ctgcagggat	2760
Thr Val	
875	
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1241.22

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<212> PRT

<213> Homo sapiens

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35 40 45
Ile Val Met Asn Cys Ala Asp Ile Asp Ile Ile Thr Ala Ser Tyr Ala
50 55 60
Pro Glu Gly Asp Glu Glu Ile His Ala Thr Gly Phe Asn Tyr Gln Asn
65 70 75 80
Glu Asp Glu Lys Val Thr Leu Ser Phe Pro Ser Thr Leu Gln Thr Gly
85 90 95
Thr Gly Thr Leu Lys Ile Asp Phe Val Gly Glu Leu Asn Asp Lys Met
100 105 110
Lys Gly Phe Tyr Arg Ser Lys Tyr Thr Thr Pro Ser Gly Glu Val Arg
115 120 125
Tyr Ala Ala Val Thr Gln Phe Glu Ala Thr Asp Ala Arg Arg Ala Phe
130 135 140
Pro Cys Trp Asp Glu Pro Ala Ile Lys Ala Thr Phe Asp Ile Ser Leu
145 150 155 160
Val Val Pro Lys Asp Arg Val Ala Leu Ser Asn Met Asn Val Ile Asp
165 170 175
Arg Lys Pro Tyr Pro Asp Asp Glu Asn Leu Val Glu Val Lys Phe Ala
180 185 190
Arg Thr Pro Val Met Ser Thr Tyr Leu Val Ala Phe Val Val Gly Glu
195 200 205

1241.22

Tyr Asp Phe Val Glu Thr Arg Ser Lys Asp Gly Val Cys Val Arg Val
 210 215 220
 Tyr Thr Pro Val Gly Lys Ala Glu Gln Gly Lys Phe Ala Leu Glu Val
 225 230 235 240
 Ala Ala Lys Thr Leu Pro Phe Tyr Lys Asp Tyr Phe Asn Val Pro Tyr
 245 250 255
 Pro Leu Pro Lys Ile Asp Leu Ile Ala Ile Ala Asp Phe Ala Ala Gly
 260 265 270
 Ala Met Glu Asn Trp Gly Leu Val Thr Tyr Arg Glu Thr Ala Leu Leu
 275 280 285
 Ile Asp Pro Lys Asn Ser Cys Ser Ser Ser Arg Gln Trp Val Ala Leu
 290 295 300
 Val Val Gly His Glu Leu Ala His Gln Trp Phe Gly Asn Leu Val Thr
 305 310 315 320
 Met Glu Trp Trp Thr His Leu Trp Leu Asn Glu Gly Phe Ala Ser Trp
 325 330 335
 Ile Glu Tyr Leu Cys Val Asp His Cys Phe Pro Glu Tyr Asp Ile Trp
 340 345 350
 Thr Gln Phe Val Ser Ala Asp Tyr Thr Arg Ala Gln Glu Leu Asp Ala
 355 360 365
 Leu Asp Asn Ser His Pro Ile Glu Val Ser Val Gly His Pro Ser Glu
 370 375 380
 Val Asp Glu Ile Phe Asp Ala Ile Ser Tyr Ser Lys Gly Ala Ser Val
 385 390 395 400
 Ile Arg Met Leu His Asp Tyr Ile Gly Asp Lys Asp Phe Lys Lys Gly
 405 410 415
 Met Asn Met Tyr Leu Thr Lys Phe Gln Gln Lys Asn Ala Ala Thr Glu
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 Asp Leu Trp Glu Ser Leu Glu Asn Ala Ser Gly Lys Pro Ile Ala Ala
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 Val Met Asn Thr Trp Thr Lys Gln Met Gly Phe Pro Leu Ile Tyr Val
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1241.22

Glu Ala Glu Gln Val Glu Asp Asp Arg Leu Leu Arg Leu Ser Gln Lys
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485 490 495
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Asp Leu Phe Ser Leu Ala Arg Ala Gly Ile Ile Ser Thr Val Glu Val
580 585 590
Leu Lys Val Met Glu Ala Phe Val Asn Glu Pro Asn Tyr Thr Val Trp
595 600 605
Ser Asp Leu Ser Cys Asn Leu Gly Ile Leu Ser Thr Leu Leu Ser His
610 615 620
Thr Asp Phe Tyr Glu Glu Ile Gln Glu Phe Val Lys Asp Val Phe Ser
625 630 635 640
Pro Ile Gly Glu Arg Leu Gly Trp Asp Pro Lys Pro Gly Glu Gly His
645 650 655
Leu Asp Ala Leu Leu Arg Gly Leu Val Leu Gly Lys Leu Gly Lys Ala
660 665 670
Gly His Lys Ala Thr Leu Glu Glu Ala Arg Arg Arg Phe Lys Asp His
675 680 685
Val Glu Gly Lys Gln Ile Leu Ser Ala Asp Leu Arg Ser Pro Val Tyr
690 695 700
Leu Thr Val Leu Lys His Gly Asp Gly Thr Thr Leu Asp Ile Met Leu

705	710	1241.22 715	720
Lys	Leu	His	Lys
Gln	Ala	Asp	Met
Gln	Glu	Glu	Lys
Asn	Arg	Ile	Glu
725	730	735	
Arg	Val	Leu	Gly
Ala	Thr	Leu	Leu
Pro	Asp	Leu	Ile
Gln	Lys	Val	Leu
740	745	750	
Thr	Phe	Ala	Leu
Ser	Glu	Glu	Val
Arg	Pro	Gln	Asp
Thr	Val	Ser	Val
755	760	765	
Ile	Gly	Gly	Val
Ala	Gly	Gly	Ser
Lys	His	Gly	Arg
Lys	Ala	Ala	Trp
770	775	780	
Lys	Phe	Ile	Lys
Asp	Asn	Trp	Glu
Glu	Leu	Tyr	Asn
Arg	Tyr	Gln	Gly
785	790	795	800
Gly	Phe	Leu	Ile
Ser	Arg	Leu	Ile
Lys	Leu	Ser	Val
Glu	Gly	Phe	Ala
805	810	815	
Val	Asp	Lys	Met
Ala	Gly	Glu	Val
Lys	Ala	Phe	Phe
Glu	Ser	His	Pro
820	825	830	
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Glu	Arg	Thr	Ile
Gln	Gln	Cys	Cys
Glu	Asn	Ile	Leu
835	840	845	
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Trp	Leu	Lys	Arg
Asp	Ala	Glu	Ser
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Pro	Thr	Val	
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<211> 2007

<212> DNA

<213> Homo sapiens

<220>

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<222> (1124)..(1330)

<400> 11

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1241.22

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Met Asp Lys Gln

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Lys His Leu Glu Val Arg Arg Ser Val Phe Lys Ile Gln Gly Lys Ile
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gcc ttc agt ctg atg ttt gtt ctc aag gac tta tcc cct aca ata ttc 1231
Ala Phe Ser Leu Met Phe Val Leu Lys Asp Leu Ser Pro Thr Ile Phe
25 30 35
tcc cac tcc ata ctt ctc ctt cta ccc cac cat gtg ctc ccg tgc act 1279
Ser His Ser Ile Leu Leu Leu Leu Pro His His Val Leu Pro Cys Thr
40 45 50
cct cag atg gtc aga ggg gta acc caa gtc ctt aga gaa ttt ggg gac 1327
Pro Gln Met Val Arg Gly Val Thr Gln Val Leu Arg Glu Phe Gly Asp
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caa tagaatatgt gatgtgtgaa ttttctttaa aaaacttaag gagtctttgc 1380

1241.22

Gln

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<212> PRT

<213> Homo sapiens

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<210> 13

<211> 1953

<212> DNA

1241.22

<213> Homo sapiens

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<222> (135)..(1850)

<400> 13

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Gly Ala Gln Ala Ser Ser Thr Pro Leu Ser Pro Thr Arg Ile Thr Arg
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Leu Gln Glu Lys Glu Asp Leu Gln Glu Leu Asn Asp Arg Leu Ala Val
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tac atc gac cgt gtg cgc tcg ctg gaa acg gag aac gca ggg ctg cgc 314
Tyr Ile Asp Arg Val Arg Ser Leu Glu Thr Glu Asn Ala Gly Leu Arg
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Leu Arg Ile Thr Glu Ser Glu Glu Val Val Ser Arg Glu Val Ser Gly
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Ile Lys Ala Ala Tyr Glu Ala Glu Leu Gly Asp Ala Arg Lys Thr Leu
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Asp Ser Val Ala Lys Glu Arg Ala Arg Leu Gln Leu Glu Leu Ser Lys
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gtg cgt gag gag ttt aag gag ctg aaa gcg cgc aat acc aag aag gag 506
Val Arg Glu Glu Phe Lys Glu Leu Lys Ala Arg Asn Thr Lys Lys Glu
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Asp	Phe	Gln	Lys	Asn	Ile	Tyr	Ser	Glu	Glu	Leu	Arg	Glu	Thr	Lys	Arg	
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Arg	His	Glu	Thr	Arg	Leu	Val	Glu	Ile	Asp	Asn	Gly	Lys	Gln	Arg	Glu	
				225					230					235		
ttt	gag	agc	cgg	ctg	gcg	gat	gcg	ctg	cag	gaa	ctg	cgg	gcc	cag	cat	890
Phe	Glu	Ser	Arg	Leu	Ala	Asp	Ala	Leu	Gln	Glu	Leu	Arg	Ala	Gln	His	
				240					245					250		
gag	gac	cag	gtg	gag	cag	tat	aag	aag	gag	ctg	gag	aag	act	tat	tct	938
Glu	Asp	Gln	Val	Glu	Gln	Tyr	Lys	Lys	Glu	Leu	Glu	Lys	Thr	Tyr	Ser	
				255					260					265		
gcc	aag	ctg	gac	aat	gcc	agg	cag	tct	gct	gag	agg	aac	agc	aac	ctg	986
Ala	Lys	Leu	Asp	Asn	Ala	Arg	Gln	Ser	Ala	Glu	Arg	Asn	Ser	Asn	Leu	
				270					275					280		
gtg	ggg	gct	gcc	cac	gag	gag	ctg	cag	cag	tcg	cgc	atc	cgc	atc	gac	1034
Val	Gly	Ala	Ala	His	Glu	Glu	Leu	Gln	Gln	Ser	Arg	Ile	Arg	Ile	Asp	

285	290	1241.22 295	300	
agc ctc tct gcc cag ctc agc cag ctc cag aag cag ctg gca gcc aag				1082
Ser Leu Ser Ala Gln Leu Ser Gln Leu Gln Lys Gln Leu Ala Ala Lys				
305	310	315		
gag gcg aag ctt cga gac ctg gag gac tca ctg gcc cgt gag cgg gac				1130
Glu Ala Lys Leu Arg Asp Leu Glu Asp Ser Leu Ala Arg Glu Arg Asp				
320	325	330		
acc agc cgg cgg ctg ctg gcg gaa aag gag cgg gag atg gcc gag atg				1178
Thr Ser Arg Arg Leu Leu Ala Glu Lys Glu Arg Glu Met Ala Glu Met				
335	340	345		
cgg gca agg atg cag cag cag ctg gac gag tac cag gag ctt ctg gac				1226
Arg Ala Arg Met Gln Gln Gln Leu Asp Glu Tyr Gln Glu Leu Leu Asp				
350	355	360		
atc aag ctg gcc ctg gac atg gag atc cac gcc tac cgc aag ctc ttg				1274
Ile Lys Leu Ala Leu Asp Met Glu Ile His Ala Tyr Arg Lys Leu Leu				
365	370	375	380	
gag ggc gag gag gag agg cta cgc ctg tcc ccc agc cct acc tcg cag				1322
Glu Gly Glu Glu Glu Arg Leu Arg Leu Ser Pro Ser Pro Thr Ser Gln				
385	390	395		
cgc agc cgt ggc cgt gct tcc tct cac tca tcc cag aca cag ggt ggg				1370
Arg Ser Arg Gly Arg Ala Ser Ser His Ser Ser Gln Thr Gln Gly Gly				
400	405	410	/	
ggc agc gtc acc aaa aag cgc aaa ctg gag tcc act gag agc cgc agc				1418
Gly Ser Val Thr Lys Lys Arg Lys Leu Glu Ser Thr Glu Ser Arg Ser				
415	420	425		
agc ttc tca cag cac gca cgc act agc ggg cgc gtg gcc gtg gag gag				1466
Ser Phe Ser Gln His Ala Arg Thr Ser Gly Arg Val Ala Val Glu Glu				
430	435	440		
gtg gat gag gag ggc aag ttt gtc cgg ctg cgc aac aag tcc aat gag				1514
Val Asp Glu Glu Gly Lys Phe Val Arg Leu Arg Asn Lys Ser Asn Glu				
445	450	455	460	
gac cag tcc atg ggc aat tgg cag atc aag cgc cag aat gga gat gat				1562

1241.22

Asp Gln Ser Met Gly Asn Trp Gln Ile Lys Arg Gln Asn Gly Asp Asp
465 470 475
ccc ttg ctg act tac cgg ttc cca cca aag ttc acc ctg aag gct ggg 1610
Pro Leu Leu Thr Tyr Arg Phe Pro Pro Lys Phe Thr Leu Lys Ala Gly
480 485 490
cag gtg gtg acg atc tgg gct gca gga gct ggg gcc acc cac agc ccc 1658
Gln Val Val Thr Ile Trp Ala Ala Gly Ala Gly Ala Thr His Ser Pro
495 500 505
cct acc gac ctg gtg tgg aag gca cag aac acc tgg ggc tgc ggg aac 1706
Pro Thr Asp Leu Val Trp Lys Ala Gln Asn Thr Trp Gly Cys Gly Asn
510 515 520
agc ctg cgt acg gct ctc atc aac tcc act ggg gaa gaa gtg gcc atg 1754
Ser Leu Arg Thr Ala Leu Ile Asn Ser Thr Gly Glu Glu Val Ala Met
525 530 535 540
cgc aag ctg gtg cgc tca gtg act gtg gtt gag gac gac gag gat gag 1802
Arg Lys Leu Val Arg Ser Val Thr Val Val Glu Asp Asp Glu Asp Glu
545 550 555
gat gga gat gac ctg ctc cat cac cac cac gtg agt ggt agc cgc cgc 1850
Asp Gly Asp Asp Leu Leu His His His His Val Ser Gly Ser Arg Arg
560 565 570
tgaggccgag cctgcactgg ggccaccagc caggcctggg ggcagcctct cccagcctc 1910
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<211> 572

<212> PRT

<213> Homo sapiens

<400> 14

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Ser Ser Thr Pro Leu Ser Pro Thr Arg Ile Thr Arg Leu Gln Glu Lys
20 25 30

1241.22

Glu Asp Leu Gln Glu Leu Asn Asp Arg Leu Ala Val Tyr Ile Asp Arg
35 40 45
Val Arg Ser Leu Glu Thr Glu Asn Ala Gly Leu Arg Leu Arg Ile Thr
50 55 60
Glu Ser Glu Glu Val Val Ser Arg Glu Val Ser Gly Ile Lys Ala Ala
65 70 75 80
Tyr Glu Ala Glu Leu Gly Asp Ala Arg Lys Thr Leu Asp Ser Val Ala
85 90 95
Lys Glu Arg Ala Arg Leu Gln Leu Glu Leu Ser Lys Val Arg Glu Glu
100 105 110
Phe Lys Glu Leu Lys Ala Arg Asn Thr Lys Lys Glu Gly Asp Leu Ile
115 120 125
Ala Ala Gln Ala Arg Leu Lys Asp Leu Glu Ala Leu Leu Asn Ser Lys
130 135 140
Glu Ala Ala Leu Ser Thr Ala Leu Ser Glu Lys Arg Thr Leu Glu Gly
145 150 155 160
Glu Leu His Asp Leu Arg Gly Gln Val Ala Lys Leu Glu Ala Ala Leu
165 170 175
Gly Glu Ala Lys Lys Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp
180 185 190
Ala Glu Asn Arg Leu Gln Thr Met Lys Glu Glu Leu Asp Phe Gln Lys
195 200 205
Asn Ile Tyr Ser Glu Glu Leu Arg Glu Thr Lys Arg Arg His Glu Thr
210 215 220
Arg Leu Val Glu Ile Asp Asn Gly Lys Gln Arg Glu Phe Glu Ser Arg
225 230 235 240
Leu Ala Asp Ala Leu Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val
245 250 255
Glu Gln Tyr Lys Lys Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp
260 265 270
Asn Ala Arg Gln Ser Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala

1241.22

275	280	285
His Glu Glu Leu Gln Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala		
290	295	300
Gln Leu Ser Gln Leu Gln Lys Gln Leu Ala Ala Lys Glu Ala Lys Leu		
305	310	315
Arg Asp Leu Glu Asp Ser Leu Ala Arg Glu Arg Asp Thr Ser Arg Arg		
325	330	335
Leu Leu Ala Glu Lys Glu Arg Glu Met Ala Glu Met Arg Ala Arg Met		
340	345	350
Gln Gln Gln Leu Asp Glu Tyr Gln Glu Leu Leu Asp Ile Lys Leu Ala		
355	360	365
Leu Asp Met Glu Ile His Ala Tyr Arg Lys Leu Leu Glu Gly Glu Glu		
370	375	380
Glu Arg Leu Arg Leu Ser Pro Ser Pro Thr Ser Gln Arg Ser Arg Gly		
385	390	395
Arg Ala Ser Ser His Ser Ser Gln Thr Gln Gly Gly Gly Ser Val Thr		
405	410	415
Lys Lys Arg Lys Leu Glu Ser Thr Glu Ser Arg Ser Ser Phe Ser Gln		
420	425	430
His Ala Arg Thr Ser Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu		
435	440	445
Gly Lys Phe Val Arg Leu Arg Asn Lys Ser Asn Glu Asp Gln Ser Met		
450	455	460
Gly Asn Trp Gln Ile Lys Arg Gln Asn Gly Asp Asp Pro Leu Leu Thr		
465	470	475
Tyr Arg Phe Pro Pro Lys Phe Thr Leu Lys Ala Gly Gln Val Val Thr		
485	490	495
Ile Trp Ala Ala Gly Ala Gly Ala Thr His Ser Pro Pro Thr Asp Leu		
500	505	510
Val Trp Lys Ala Gln Asn Thr Trp Gly Cys Gly Asn Ser Leu Arg Thr		
515	520	525
Ala Leu Ile Asn Ser Thr Gly Glu Glu Val Ala Met Arg Lys Leu Val		

1241.22

530

535

540

Arg Ser Val Thr Val Val Glu Asp Asp Glu Asp Glu Asp Gly Asp Asp

545

550

555

560

Leu Leu His His His His Val Ser Gly Ser Arg Arg

565

570

<210> 15

<211> 2865

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (240)..(1475)

<220>

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1781, 1804, 1805, 1807, 1809, 1812, 2317, 2534,
2726, 2728, 2746, 2751, 2785, 2788, 2797, 2801,
2813, 2816, 2827, 2828, 2859, 2963, 2964,

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gagctcagac tcagaggaac atctgctggag agacccccga agccctctcc agggcagtcc 180
tcatccagac gctccgtagg tgcagacagg agcgcgcagt ggccccggct cgccgcgcc 239
atg gag cgg atc ccc agc gcg caa cca ccc ccc gcc tgc ctg ccc aaa 287
Met Glu Arg Ile Pro Ser Ala Gln Pro Pro Pro Ala Cys Leu Pro Lys

1

5

10

15

gca ccg gga ctg gag cac cga gac cta cca ggg atg tac cct gcc cac 335
Ala Pro Gly Leu Glu His Arg Asp Leu Pro Gly Met Tyr Pro Ala His

20

25

30

atg tac caa gtg tac aag tca aga cgg gga ata aag cgg agc gag gac 383
Met Tyr Gln Val Tyr Lys Ser Arg Arg Gly Ile Lys Arg Ser Glu Asp

1241.22

35	40	45	
agc aag gag acc tac aaa ttg ccg cac cgg ctc ttc gag aaa aag aga	431		
Ser Lys Glu Thr Tyr Lys Leu Pro His Arg Leu Phe Glu Lys Lys Arg			
50	55	60	
cgt gac cgg att aac gag tgc atc gcc cag ctg aag gat ctc cta ccc	479		
Arg Asp Arg Ile Asn Glu Cys Ile Ala Gln Leu Lys Asp Leu Leu Pro			
65	70	75	80
gaa cat ctc aaa ctt aca act ttg ggt cac ttg gaa aaa gca gtg gtt	527		
Glu His Leu Lys Leu Thr Thr Leu Gly His Leu Glu Lys Ala Val Val			
85	90	95	
ctt gaa ctt acc ttg aag cat gtg aaa gca cta aca aac cta att gat	575		
Leu Glu Leu Thr Leu Lys His Val Lys Ala Leu Thr Asn Leu Ile Asp			
100	105	110	
cag cag cag cag aaa atc att gcc ctg cag agt ggt tta caa gct ggt	623		
Gln Gln Gln Gln Lys Ile Ile Ala Leu Gln Ser Gly Leu Gln Ala Gly			
115	120	125	
gag ctg tca ggg aga aat gtc gaa aca ggt caa gag atg ttc tgc tca	671		
Glu Leu Ser Gly Arg Asn Val Glu Thr Gly Gln Glu Met Phe Cys Ser			
130	135	140	
ggc ttc cag aca tgt gcc cgg gag gtg ctt cag tat ctg gcc aag cac	719		
Gly Phe Gln Thr Cys Ala Arg Glu Val Leu Gln Tyr Leu Ala Lys His			
145	150	155	160
gag aac act cgg gac ctg aag tct tcg cag ctt gtc acc cac ctc cac	767		
Glu Asn Thr Arg Asp Leu Lys Ser Ser Gln Leu Val Thr His Leu His			
165	170	175	
cgg gtg gtc tcg gag ctg ctg cag ggt ggt acc tcc agg aag cca tca	815		
Arg Val Val Ser Glu Leu Leu Gln Gly Gly Thr Ser Arg Lys Pro Ser			
180	185	190	
gac cca gct ccc aaa gtg atg gac ttc aag gaa aaa ccc agc tct ccg	863		
Asp Pro Ala Pro Lys Val Met Asp Phe Lys Glu Lys Pro Ser Ser Pro			
195	200	205	

1241.22

gcc aaa ggt tgc gaa ggt cct ggg aaa aac tgc gtg cca gtc atc cag	911
Ala Lys Gly Ser Glu Gly Pro Gly Lys Asn Cys Val Pro Val Ile Gln	
210 215 220	
cgg act ttc gct cac tgc agt ggg gag cag agc ggc agc gac acg gac	959
Arg Thr Phe Ala His Ser Ser Gly Glu Gln Ser Gly Ser Asp Thr Asp	
225 230 235 240	
aca gac agt ggc tat gga gga gat tgc gag aag ggc gac ttg cgc agt	1007
Thr Asp Ser Gly Tyr Gly Gly Asp Ser Glu Lys Gly Asp Leu Arg Ser	
245 250 255	
gag cag ccg tgc ttc aaa agt gac cac gga cgc agg ttc acg atg gga	1055
Glu Gln Pro Cys Phe Lys Ser Asp His Gly Arg Arg Phe Thr Met Gly	
260 265 270	
gaa agg atc ggc gca att aag caa gag tcc gaa gaa ccc ccc aca aaa	1103
Glu Arg Ile Gly Ala Ile Lys Gln Glu Ser Glu Glu Pro Pro Thr Lys	
275 280 285	
aag aac cgg atg cag ctt tgc gat gat gaa ggc cat ttc act agc agt	1151
Lys Asn Arg Met Gln Leu Ser Asp Asp Glu Gly His Phe Thr Ser Ser	
290 295 300	
gac ctg atc agc tcc ccg ttc ctg ggc cca cac cca cac cag cct cct	1199
Asp Leu Ile Ser Ser Pro Phe Leu Gly Pro His Pro His Gln Pro Pro	
305 310 315 320	
ttc tgc ctg ccc ttc tac ctg atc cca cct tca gcg act gcc tac ctg	1247
Phe Cys Leu Pro Phe Tyr Leu Ile Pro Pro Ser Ala Thr Ala Tyr Leu	
325 330 335	
ccc atg ctg gag aag tgc tgg tat ccc acc tca gtg cca gtg cta tac	1295
Pro Met Leu Glu Lys Cys Trp Tyr Pro Thr Ser Val Pro Val Leu Tyr	
340 345 350	
cca ggc ctc aac gcc tct gcc gca gcc ctc tct agc ttc atg aac cca	1343
Pro Gly Leu Asn Ala Ser Ala Ala Ala Leu Ser Ser Phe Met Asn Pro	
355 360 365	
gac aag atc tgc gct ccc ttg ctc atg ccc cag aga ctc cct tct ccc	1391
Asp Lys Ile Ser Ala Pro Leu Leu Met Pro Gln Arg Leu Pro Ser Pro	

1241.22

370	375	380	
ttg cca gct cat ccg tcc gtc gac tct tct gtc ttg ctc caa gct ctg	1439		
Leu Pro Ala His Pro Ser Val Asp Ser Ser Val Leu Leu Gln Ala Leu			
385	390	395	400
aag cca atc ccc cct tta aac tta gaa acc aaa gac taaactctct	1485		
Lys Pro Ile Pro Pro Leu Asn Leu Glu Thr Lys Asp			
405	410		
aggggatcct gctgcttngc tttcctncct cgctacttcc taaaaagcaa ccnnaaagnt	1545		
ttngtgaatg ctggnagant gttgcattgt gtatactgag ataacttgag gcatggagag	1605		
caganncagg gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gtatgtgcgt gtgcgtgcac	1665		
atgtgtgcct gcgtgttgggt ataggacttt anngctcctt nnggcatagg gaagtcacga	1725		
aggattgctn gacatcagga gactnggggg ggattgtagc agacgtctgg gcttnncccc	1785		
accagagaa tagcccccnn cnanacanat cagctggatt tacaaaagct tcaaagtctt	1845		
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tcaaaagagg gctttccagg gctcagctcc caaccagctg ttaggacccc acccttttgc	1965		
ctttattgtc gacgtgactc accagacgtc ggggagagag agcagtcaga ccgagctttt	2025		
ctgctaacat ggggagggta gcagacactg gcatagcacg gtagtggttt gggggaggggt	2085		
ttccgcagggt ctgctcccca cccctgcctc ggaagaataa agagaatgta gttccctact	2145		
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gctgccccgg agggagggag gagttccctg ggcttctggc acctgtttct aggcctaacc	2265		
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agttttcaat tccatcctaa aactcctttt aaccaagctt agcttctcaa agggctaacc	2445		
aagccttggg accgccagat cttttctgta ggctaattcc tcttggccaa cggcatatgg	2505		
agtgtcctta ttgctaaaaa ggattccgnc tccttcaaag aagttttatt tttgggtccag	2565		
agtacttggt ttcccgatgt gtccagccag ctccgcagca gcttttcaa atgcactatg	2625		
cctgattgct gatcgtgttt taactttttc ttttcctgtt tttattttgg tattaagtcg	2685		
ctggctttat ttgtaaagct gttataaata tatattatat naantatatt aaaaaggaaa	2745		
ntgttncaga tgtttatttg tataattact tgattcacan agngagaaaa antgantgta	2805		
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<211> 412

<212> PRT

<213> Homo sapiens

<400> 16

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Ala Pro Gly Leu Glu His Arg Asp Leu Pro Gly Met Tyr Pro Ala His
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Met Tyr Gln Val Tyr Lys Ser Arg Arg Gly Ile Lys Arg Ser Glu Asp
35 40 45
Ser Lys Glu Thr Tyr Lys Leu Pro His Arg Leu Phe Glu Lys Lys Arg
50 55 60
Arg Asp Arg Ile Asn Glu Cys Ile Ala Gln Leu Lys Asp Leu Leu Pro
65 70 75 80
Glu His Leu Lys Leu Thr Thr Leu Gly His Leu Glu Lys Ala Val Val
85 90 95
Leu Glu Leu Thr Leu Lys His Val Lys Ala Leu Thr Asn Leu Ile Asp
100 105 110
Gln Gln Gln Gln Lys Ile Ile Ala Leu Gln Ser Gly Leu Gln Ala Gly
115 120 125
Glu Leu Ser Gly Arg Asn Val Glu Thr Gly Gln Glu Met Phe Cys Ser
130 135 140
Gly Phe Gln Thr Cys Ala Arg Glu Val Leu Gln Tyr Leu Ala Lys His
145 150 155 160
Glu Asn Thr Arg Asp Leu Lys Ser Ser Gln Leu Val Thr His Leu His
165 170 175
Arg Val Val Ser Glu Leu Leu Gln Gly Gly Thr Ser Arg Lys Pro Ser
180 185 190
Asp Pro Ala Pro Lys Val Met Asp Phe Lys Glu Lys Pro Ser Ser Pro
195 200 205
Ala Lys Gly Ser Glu Gly Pro Gly Lys Asn Cys Val Pro Val Ile Gln

1241.22
 220
 210 215
 Arg Thr Phe Ala His Ser Ser Gly Glu Gln Ser Gly Ser Asp Thr Asp
 225 230 235 240
 Thr Asp Ser Gly Tyr Gly Gly Asp Ser Glu Lys Gly Asp Leu Arg Ser
 245 250 255
 Glu Gln Pro Cys Phe Lys Ser Asp His Gly Arg Arg Phe Thr Met Gly
 260 265 270
 Glu Arg Ile Gly Ala Ile Lys Gln Glu Ser Glu Glu Pro Pro Thr Lys
 275 280 285
 Lys Asn Arg Met Gln Leu Ser Asp Asp Glu Gly His Phe Thr Ser Ser
 290 295 300
 Asp Leu Ile Ser Ser Pro Phe Leu Gly Pro His Pro His Gln Pro Pro
 305 310 315 320
 Phe Cys Leu Pro Phe Tyr Leu Ile Pro Pro Ser Ala Thr Ala Tyr Leu
 325 330 335
 Pro Met Leu Glu Lys Cys Trp Tyr Pro Thr Ser Val Pro Val Leu Tyr
 340 345 350
 Pro Gly Leu Asn Ala Ser Ala Ala Ala Leu Ser Ser Phe Met Asn Pro
 355 360 365
 Asp Lys Ile Ser Ala Pro Leu Leu Met Pro Gln Arg Leu Pro Ser Pro
 370 375 380
 Leu Pro Ala His Pro Ser Val Asp Ser Ser Val Leu Leu Gln Ala Leu
 385 390 395 400
 Lys Pro Ile Pro Pro Leu Asn Leu Glu Thr Lys Asp
 405 410

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<212> DNA

<213> Homo sapiens

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<221> CDS

1241.22

<222> (164)..(2665)

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tcttaactag tgtaggaaaa cggctcaacc caccgctgcc gaa atg aag tat aag 175

Met Lys Tyr Lys

1

aat ctt atg gca agg gcc tta tat gac aat gtc cca gag tgt gcc gag 223
Asn Leu Met Ala Arg Ala Leu Tyr Asp Asn Val Pro Glu Cys Ala Glu

5

10

15

20

gaa ctg gcc ttt cgc aag gga gac atc ctg acc gtc ata gag cag aac 271
Glu Leu Ala Phe Arg Lys Gly Asp Ile Leu Thr Val Ile Glu Gln Asn

25

30

35

aca ggg gga ctg gaa gga tgg tgg ctg tgc tcg tta cac ggt cgg caa 319
Thr Gly Gly Leu Glu Gly Trp Trp Leu Cys Ser Leu His Gly Arg Gln

40

45

50

ggc att gtc cca ggc aac cgg gtg aag ctt ctg att ggt ccc atg cag 367
Gly Ile Val Pro Gly Asn Arg Val Lys Leu Leu Ile Gly Pro Met Gln

55

60

65

gag act gcc tcc agt cac gag cag cct gcc tct gga ctg atg cag cag 415
Glu Thr Ala Ser Ser His Glu Gln Pro Ala Ser Gly Leu Met Gln Gln

70

75

80

acc ttt ggc caa cag aag ctc tat caa gtg cca aac cca cag gct gct 463
Thr Phe Gly Gln Gln Lys Leu Tyr Gln Val Pro Asn Pro Gln Ala Ala

85

90

95

100

ccc cga gac acc atc tac caa gtg cca cct tcc tac caa aat cag gga 511
Pro Arg Asp Thr Ile Tyr Gln Val Pro Pro Ser Tyr Gln Asn Gln Gly

105

110

115

att tac caa gtc ccc act ggc cac ggc acc caa gaa caa gag gta tat 559
Ile Tyr Gln Val Pro Thr Gly His Gly Thr Gln Glu Gln Glu Val Tyr

120

125

130

cag gtg cca cca tca gtg cag aga agc att ggg gga acc agt ggg ccc 607

1241.22

Gln Val Pro Pro Ser Val Gln Arg Ser Ile Gly Gly Thr Ser Gly Pro	
135 140 145	
cac gtg ggt aaa aag gtg ata acc ccc gtg agg aca ggc cat ggc tac	655
His Val Gly Lys Lys Val Ile Thr Pro Val Arg Thr Gly His Gly Tyr	
150 155 160	
gta tac gag tac cca tcc aga tac caa aag gat gtc tat gat atc cct	703
Val Tyr Glu Tyr Pro Ser Arg Tyr Gln Lys Asp Val Tyr Asp Ile Pro	
165 170 175 180	
cct tct cat acc act caa ggg gta tac gac atc cct ccc tca tca gca	751
Pro Ser His Thr Thr Gln Gly Val Tyr Asp Ile Pro Pro Ser Ser Ala	
185 190 195	
aaa ggc cct gtg ttt tca gtt cca gtg gga gag ata aaa cct caa ggg	799
Lys Gly Pro Val Phe Ser Val Pro Val Gly Glu Ile Lys Pro Gln Gly	
200 205 210	
gtg tat gac atc ccg cct aca aaa ggg gta tat gcc att ccg ccc tct	847
Val Tyr Asp Ile Pro Pro Thr Lys Gly Val Tyr Ala Ile Pro Pro Ser	
215 220 225	
gct tgc cgg gat gaa gca ggg ctt agg gaa aaa gac tat gac ttc ccc	895
Ala Cys Arg Asp Glu Ala Gly Leu Arg Glu Lys Asp Tyr Asp Phe Pro	
230 235 240	
cct ccc atg aga caa gct gga agg ccg gac ctc aga ccg gag ggg gtt	943
Pro Pro Met Arg Gln Ala Gly Arg Pro Asp Leu Arg Pro Glu Gly Val	
245 250 255 260	
tat gac att cct cca acc tgc acc aag cca gca ggg aag gac ctt cat	991
Tyr Asp Ile Pro Pro Thr Cys Thr Lys Pro Ala Gly Lys Asp Leu His	
265 270 275	
gta aaa tac aac tgt gac att cca gga gct gca gaa ccg gtg gct cga	1039
Val Lys Tyr Asn Cys Asp Ile Pro Gly Ala Ala Glu Pro Val Ala Arg	
280 285 290	
agg cac cag agc ctg tcc ccg aat cac cca ccc ccg caa ctc gga cag	1087
Arg His Gln Ser Leu Ser Pro Asn His Pro Pro Pro Gln Leu Gly Gln	

1241.22

295	300	305	
tca gtg ggc tct cag aac gac gca tat gat gtc ccc cga ggc gtt cag			1135
Ser Val Gly Ser Gln Asn Asp Ala Tyr Asp Val Pro Arg Gly Val Gln			
310	315	320	
ttt ctt gag cca cca gca gaa acc agt gag aaa gca aac ccc cag gaa			1183
Phe Leu Glu Pro Pro Ala Glu Thr Ser Glu Lys Ala Asn Pro Gln Glu			
325	330	335	340
agg gat ggt gtt tat gat gtc cct ctg cat aac ccg cca gat gct aaa			1231
Arg Asp Gly Val Tyr Asp Val Pro Leu His Asn Pro Pro Asp Ala Lys			
345	350	355	
ggc tct cgg gac ttg gtg gat ggg atc aac cga ttg tct ttc tcc agt			1279
Gly Ser Arg Asp Leu Val Asp Gly Ile Asn Arg Leu Ser Phe Ser Ser			
360	365	370	
aca ggc agc acc cgg agt aac atg tcc acg tct tcc acc tcc tcc aag			1327
Thr Gly Ser Thr Arg Ser Asn Met Ser Thr Ser Ser Thr Ser Ser Lys			
375	380	385	
gag tcc tca ctg tca gcc tcc cca gct cag gac aaa agg ctc ttc ctg			1375
Glu Ser Ser Leu Ser Ala Ser Pro Ala Gln Asp Lys Arg Leu Phe Leu			
390	395	400	
gat cca gac aca gct att gag aga ctt cag cgg ctc cag cag gcc ctt			1423
Asp Pro Asp Thr Ala Ile Glu Arg Leu Gln Arg Leu Gln Gln Ala Leu			
405	410	415	420
gag atg ggt gtc tcc agc cta atg gca ctg gtc act acc gac tgg cgg			1471
Glu Met Gly Val Ser Ser Leu Met Ala Leu Val Thr Thr Asp Trp Arg			
425	430	435	
tgt tac gga tat atg gaa aga cac atc aat gaa ata cgc aca gca gtg			1519
Cys Tyr Gly Tyr Met Glu Arg His Ile Asn Glu Ile Arg Thr Ala Val			
440	445	450	
gac aag gtg gag ctg ttc ctg aag gag tac ctc cac ttt gtc aag gga			1567
Asp Lys Val Glu Leu Phe Leu Lys Glu Tyr Leu His Phe Val Lys Gly			
455	460	465	
gct gtt gca aat gct gcc tgc ctc ccg gaa ctc atc ctc cac aac aag			1615

1241.22

Ala Val Ala Asn Ala Ala Cys Leu Pro Glu Leu Ile Leu His Asn Lys	
470 475 480	
atg aag cgg gag ctg caa cga gtc gaa gac tcc cac cag atc ctg agt	1663
Met Lys Arg Glu Leu Gln Arg Val Glu Asp Ser His Gln Ile Leu Ser	
485 490 495 500	
caa acc agc cat gac tta aat gag tgc agc tgg tcc ctg aat atc ttg	1711
Gln Thr Ser His Asp Leu Asn Glu Cys Ser Trp Ser Leu Asn Ile Leu	
505 510 515	
gcc atc aac aag ccc cag aac aag tgt gac gat ctg gac cgg ttt gtg	1759
Ala Ile Asn Lys Pro Gln Asn Lys Cys Asp Asp Leu Asp Arg Phe Val	
520 525 530	
atg gtg gca aag acg gtg ccc gat gac gcc aag cag ctc acc aca acc	1807
Met Val Ala Lys Thr Val Pro Asp Asp Ala Lys Gln Leu Thr Thr Thr	
535 540 545	
atc aac acc aac gca gag gcc ctc ttc aga ccc ggc cct ggc agc ttg	1855
Ile Asn Thr Asn Ala Glu Ala Leu Phe Arg Pro Gly Pro Gly Ser Leu	
550 555 560	
cat ctg aag aat ggg ccg gag agc atc atg aac tca acg gag tac cca	1903
His Leu Lys Asn Gly Pro Glu Ser Ile Met Asn Ser Thr Glu Tyr Pro	
565 570 575 580	
cac ggt ggc tcc cag gga cag ctg ctg cat cct ggt gac cac aag gcc	1951
His Gly Gly Ser Gln Gly Gln Leu Leu His Pro Gly Asp His Lys Ala	
585 590 595	
cag gcc cac aac aag gca ctg ccc cca ggc ctg agc aag gag cag gcc	1999
Gln Ala His Asn Lys Ala Leu Pro Pro Gly Leu Ser Lys Glu Gln Ala	
600 605 610	
cct gac tgt agc agc agt gat ggt tct gag agg agc tgg atg gat gac	2047
Pro Asp Cys Ser Ser Ser Asp Gly Ser Glu Arg Ser Trp Met Asp Asp	
615 620 625	
tac gat tac gtc cac cta cag ggt aag gag gag ttt gag agg caa cag	2095
Tyr Asp Tyr Val His Leu Gln Gly Lys Glu Glu Phe Glu Arg Gln Gln	

1241.22

630	635	640	
aaa gag cta ttg gaa aaa gag aat atc atg aaa cag aac aag atg cag	2143		
Lys Glu Leu Leu Glu Lys Glu Asn Ile Met Lys Gln Asn Lys Met Gln			
645	650	655	660
ctg gaa cat cat cag ctg agc cag ttc cag ctg ttg gaa caa gag att	2191		
Leu Glu His His Gln Leu Ser Gln Phe Gln Leu Leu Glu Gln Glu Ile			
665	670	675	
aca aag ccc gtg gag aat gac atc tcg aag tgg aag ccc tct cag agc	2239		
Thr Lys Pro Val Glu Asn Asp Ile Ser Lys Trp Lys Pro Ser Gln Ser			
680	685	690	
cta ccc acc aca aac agt ggc gtg agt gct cag gat cgg cag ttg ctg	2287		
Leu Pro Thr Thr Asn Ser Gly Val Ser Ala Gln Asp Arg Gln Leu Leu			
695	700	705	
tgc ttc tac tat gac caa tgt gag acc cat ttc att tcc ctt ctc aac	2335		
Cys Phe Tyr Tyr Asp Gln Cys Glu Thr His Phe Ile Ser Leu Leu Asn			
710	715	720	
gcc att gac gca ctc ttc agt tgt gtc agc tca gcc cag ccc ccg cga	2383		
Ala Ile Asp Ala Leu Phe Ser Cys Val Ser Ser Ala Gln Pro Pro Arg			
725	730	735	740
atc ttc gtg gca cac agc aag ttt gtc atc ctc agt gca cac aaa ctg	2431		
Ile Phe Val Ala His Ser Lys Phe Val Ile Leu Ser Ala His Lys Leu			
745	750	755	
gtg ttc att gga gac acg ctg aca cgg cag gtg act gcc cag gac att	2479		
Val Phe Ile Gly Asp Thr Leu Thr Arg Gln Val Thr Ala Gln Asp Ile			
760	765	770	
cgc aac aaa gtc atg aac tcc agc aac cag ctc tgc gag cag ctc aag	2527		
Arg Asn Lys Val Met Asn Ser Ser Asn Gln Leu Cys Glu Gln Leu Lys			
775	780	785	
act ata gtc atg gca acc aag atg gcc gcc ctc cat tac ccc agc acc	2575		
Thr Ile Val Met Ala Thr Lys Met Ala Ala Leu His Tyr Pro Ser Thr			
790	795	800	
acg gcc ctg cag gaa atg gtg cac caa gtg aca gac ctt tct aga aat	2623		

1241.22

Thr Ala Leu Gln Glu Met Val His Gln Val Thr Asp Leu Ser Arg Asn

805 810 815 820

gcc cag ctg ttc aag cgc tct ttg ctg gag atg gca acg ttc 2665

Ala Gln Leu Phe Lys Arg Ser Leu Leu Glu Met Ala Thr Phe

825 830

tgagaagaaa aaaaagagga aggggactgc gttaacgggt actaaggaaa actggaaata 2725

ctgtctgggt ttgttaaagt ttatctatct ttgtagataa ttttatataa aaatgaaata 2785

ttttaacatt ttatgggtca gacaactttc agaaattcag ggagctggag agggaaatct 2845

ttttttcccc cctgagtgtt cttatgtata cacagaagta tctgagacat aaactgtaca 2905

gaaaacttgt ccacgtcctt ttgtatgccc atgtattcat gtttttggtt gtagatgttt 2965

gtctgatgca ttccattaaa aaaaaaacca tgaattacga agcaccttag taagcacctt 3025

ctaattgctgc attttttttg ttgttggtta aaacatccag ctgggtataa tattgttctc 3085

cacgtccttg tgatgattct gagcctggca ctgggaatct gggaagcata gtttatttgc 3145

aagtgttcac cttccaaatc atgaggcata gcatgactta ttcttggttt gaaaactctt 3205

ttcaaaactg accatcttaa acacatgatg gccaaagtgc acaaagccct cttgcggaga 3265

catttacgaa tatatatgtg gatccaagtc tcgatagtta ggcgttgag ggaagagaga 3325

ccagagagtt tagaggccag gaccacagtt aggattgggt tgtttcaata ctgagagaca 3385

gctacaataa aaggagagca attgcctccc tggggctggt caatcttctg catttgtag 3445

tgggttcagtc atgaggtttt ccaaagatg tttttagagt tgtaaaaacc atatttgcag 3505

caaagattta caaaggcgta tcagactatg attgttcacc aaaatagggg aatgggttga 3565

tccgccagtt gcaagtagag gcctttctga ctcttaatat tcactttggt gctactaccc 3625

ccattacctg aggaactggc caggtccttg atcatggaac tatagagcta ccagacatat 3685

cctgctctct aagggaaatt attgctatct tgcaccttct ttaaaactca aaaaacatat 3745

gcagacctga cactcaagag tggctagcta cacagagtcc atctaatttt tgcaacttcc 3805

ccccccgaat tc 3817

<210> 18

<211> 834

<212> PRT

<213> Homo sapiens

<400> 18

Met Lys Tyr Lys Asn Leu Met Ala Arg Ala Leu Tyr Asp Asn Val Pro

1241.22

1	5	10	15
Glu Cys Ala Glu Glu Leu Ala Phe Arg Lys Gly Asp Ile Leu Thr Val			
20	25	30	
Ile Glu Gln Asn Thr Gly Gly Leu Glu Gly Trp Trp Leu Cys Ser Leu			
35	40	45	
His Gly Arg Gln Gly Ile Val Pro Gly Asn Arg Val Lys Leu Leu Ile			
50	55	60	
Gly Pro Met Gln Glu Thr Ala Ser Ser His Glu Gln Pro Ala Ser Gly			
65	70	75	80
Leu Met Gln Gln Thr Phe Gly Gln Gln Lys Leu Tyr Gln Val Pro Asn			
85	90	95	
Pro Gln Ala Ala Pro Arg Asp Thr Ile Tyr Gln Val Pro Pro Ser Tyr			
100	105	110	
Gln Asn Gln Gly Ile Tyr Gln Val Pro Thr Gly His Gly Thr Gln Glu			
115	120	125	
Gln Glu Val Tyr Gln Val Pro Pro Ser Val Gln Arg Ser Ile Gly Gly			
130	135	140	
Thr Ser Gly Pro His Val Gly Lys Lys Val Ile Thr Pro Val Arg Thr			
145	150	155	160
Gly His Gly Tyr Val Tyr Glu Tyr Pro Ser Arg Tyr Gln Lys Asp Val			
165	170	175	
Tyr Asp Ile Pro Pro Ser His Thr Thr Gln Gly Val Tyr Asp Ile Pro			
180	185	190	
Pro Ser Ser Ala Lys Gly Pro Val Phe Ser Val Pro Val Gly Glu Ile			
195	200	205	
Lys Pro Gln Gly Val Tyr Asp Ile Pro Pro Thr Lys Gly Val Tyr Ala			
210	215	220	
Ile Pro Pro Ser Ala Cys Arg Asp Glu Ala Gly Leu Arg Glu Lys Asp			
225	230	235	240
Tyr Asp Phe Pro Pro Pro Met Arg Gln Ala Gly Arg Pro Asp Leu Arg			
245	250	255	

1241.22

Pro Glu Gly Val Tyr Asp Ile Pro Pro Thr Cys Thr Lys Pro Ala Gly
 260 265 270
 Lys Asp Leu His Val Lys Tyr Asn Cys Asp Ile Pro Gly Ala Ala Glu
 275 280 285
 Pro Val Ala Arg Arg His Gln Ser Leu Ser Pro Asn His Pro Pro Pro
 290 295 300
 Gln Leu Gly Gln Ser Val Gly Ser Gln Asn Asp Ala Tyr Asp Val Pro
 305 310 315 320
 Arg Gly Val Gln Phe Leu Glu Pro Pro Ala Glu Thr Ser Glu Lys Ala
 325 330 335
 Asn Pro Gln Glu Arg Asp Gly Val Tyr Asp Val Pro Leu His Asn Pro
 340 345 350
 Pro Asp Ala Lys Gly Ser Arg Asp Leu Val Asp Gly Ile Asn Arg Leu
 355 360 365
 Ser Phe Ser Ser Thr Gly Ser Thr Arg Ser Asn Met Ser Thr Ser Ser
 370 375 380
 Thr Ser Ser Lys Glu Ser Ser Leu Ser Ala Ser Pro Ala Gln Asp Lys
 385 390 395 400
 Arg Leu Phe Leu Asp Pro Asp Thr Ala Ile Glu Arg Leu Gln Arg Leu
 405 410 415
 Gln Gln Ala Leu Glu Met Gly Val Ser Ser Leu Met Ala Leu Val Thr
 420 425 430
 Thr Asp Trp Arg Cys Tyr Gly Tyr Met Glu Arg His Ile Asn Glu Ile
 435 440 445
 Arg Thr Ala Val Asp Lys Val Glu Leu Phe Leu Lys Glu Tyr Leu His
 450 455 460
 Phe Val Lys Gly Ala Val Ala Asn Ala Ala Cys Leu Pro Glu Leu Ile
 465 470 475 480
 Leu His Asn Lys Met Lys Arg Glu Leu Gln Arg Val Glu Asp Ser His
 485 490 495
 Gln Ile Leu Ser Gln Thr Ser His Asp Leu Asn Glu Cys Ser Trp Ser
 500 505 510

1241.22

Leu Asn Ile Leu Ala Ile Asn Lys Pro Gln Asn Lys Cys Asp Asp Leu
515 520 525
Asp Arg Phe Val Met Val Ala Lys Thr Val Pro Asp Asp Ala Lys Gln
530 535 540
Leu Thr Thr Thr Ile Asn Thr Asn Ala Glu Ala Leu Phe Arg Pro Gly
545 550 555 560
Pro Gly Ser Leu His Leu Lys Asn Gly Pro Glu Ser Ile Met Asn Ser
565 570 575
Thr Glu Tyr Pro His Gly Gly Ser Gln Gly Gln Leu Leu His Pro Gly
580 585 590
Asp His Lys Ala Gln Ala His Asn Lys Ala Leu Pro Pro Gly Leu Ser
595 600 605
Lys Glu Gln Ala Pro Asp Cys Ser Ser Ser Asp Gly Ser Glu Arg Ser
610 615 620
Trp Met Asp Asp Tyr Asp Tyr Val His Leu Gln Gly Lys Glu Glu Phe
625 630 635 640
Glu Arg Gln Gln Lys Glu Leu Leu Glu Lys Glu Asn Ile Met Lys Gln
645 650 655
Asn Lys Met Gln Leu Glu His His Gln Leu Ser Gln Phe Gln Leu Leu
660 665 670
Glu Gln Glu Ile Thr Lys Pro Val Glu Asn Asp Ile Ser Lys Trp Lys
675 680 685
Pro Ser Gln Ser Leu Pro Thr Thr Asn Ser Gly Val Ser Ala Gln Asp
690 695 700
Arg Gln Leu Leu Cys Phe Tyr Tyr Asp Gln Cys Glu Thr His Phe Ile
705 710 715 720
Ser Leu Leu Asn Ala Ile Asp Ala Leu Phe Ser Cys Val Ser Ser Ala
725 730 735
Gln Pro Pro Arg Ile Phe Val Ala His Ser Lys Phe Val Ile Leu Ser
740 745 750
Ala His Lys Leu Val Phe Ile Gly Asp Thr Leu Thr Arg Gln Val Thr

1241.22

755	760	765
Ala Gln Asp Ile Arg Asn Lys Val Met Asn Ser Ser Asn Gln Leu Cys		
770	775	780
Glu Gln Leu Lys Thr Ile Val Met Ala Thr Lys Met Ala Ala Leu His		
785	790	795
Tyr Pro Ser Thr Thr Ala Leu Gln Glu Met Val His Gln Val Thr Asp		
	805	810
Leu Ser Arg Asn Ala Gln Leu Phe Lys Arg Ser Leu Leu Glu Met Ala		
	820	830
Thr Phe		

<210> 19

<211> 567

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (36)..(506)

<400> 19

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Met Leu Ala Gly Asn Glu	
1 5	
ttc cag gtg tcc ctg agc agc tcc atg tcg gtg tca gag ctg aag gcg	101
Phe Gln Val Ser Leu Ser Ser Ser Met Ser Val Ser Glu Leu Lys Ala	
10 15 20	
cag atc acc cag aac att ggc gtg cac gcc ttc cag cag cgt ctg gct	149
Gln Ile Thr Gln Asn Ile Gly Val His Ala Phe Gln Gln Arg Leu Ala	
25 30 35	
gtc cac ccg agc ggt gtg gcg ctg cag gac agg gtc ccc ctt gcc agc	197
Val His Pro Ser Gly Val Ala Leu Gln Asp Arg Val Pro Leu Ala Ser	
40 45 50	
cag ggc ctg ggc cct ggc agc acg gtc ctg ctg gtg gtg gac aaa tgc	245

1241.22

Gln Gly Leu Gly Pro Gly Ser Thr Val	Leu Leu Val Val	Asp Lys Cys	
55	60	65	70
gac gaa cct ctg agc atc ctg gtg agg aat aac aag ggc cgc agc agc			293
Asp Glu Pro Leu Ser Ile Leu Val Arg Asn Asn Lys Gly Arg Ser Ser			
75	80	85	
acc tac gag gtg cgg ctg acg cag acc gtg gcc cac ctg aag cag caa			341
Thr Tyr Glu Val Arg Leu Thr Gln Thr Val Ala His Leu Lys Gln Gln			
90	95	100	
gtg agc ggg ctg gag ggt gtg cag gac gac ctg ttc tgg ctg acc ttc			389
Val Ser Gly Leu Glu Gly Val Gln Asp Asp Leu Phe Trp Leu Thr Phe			
105	110	115	
gag ggg aag ccc ctg gag gac cag ctc ccg ctg ggg gag tac ggc ctc			437
Glu Gly Lys Pro Leu Glu Asp Gln Leu Pro Leu Gly Glu Tyr Gly Leu			
120	125	130	
aag ccc ctg agc acc gtg ttc atg aat ctg cgc ctg cgg gga ggc ggc			485
Lys Pro Leu Ser Thr Val Phe Met Asn Leu Arg Leu Arg Gly Gly Gly			
135	140	145	150
aca gag cct ggc ggg cgg agc taagggcctc caccagcatc cgagcaggat			536
Thr Glu Pro Gly Gly Arg Ser			
155			
caagggccgg aataaaggct gttgtaagag a			567

<210> 20

<211> 157

<212> PRT

<213> Homo sapiens

<400> 20

Met Leu Ala Gly Asn Glu Phe Gln Val Ser Leu Ser Ser Ser Met Ser			
1	5	10	15
Val Ser Glu Leu Lys Ala Gln Ile Thr Gln Asn Ile Gly Val His Ala			
20	25	30	
Phe Gln Gln Arg Leu Ala Val His Pro Ser Gly Val Ala Leu Gln Asp			

1241.22

35	40	45
Arg Val Pro Leu Ala Ser Gln Gly Leu Gly Pro Gly Ser Thr Val Leu		
50	55	60
Leu Val Val Asp Lys Cys Asp Glu Pro Leu Ser Ile Leu Val Arg Asn		
65	70	75
Asn Lys Gly Arg Ser Ser Thr Tyr Glu Val Arg Leu Thr Gln Thr Val		
85	90	95
Ala His Leu Lys Gln Gln Val Ser Gly Leu Glu Gly Val Gln Asp Asp		
100	105	110
Leu Phe Trp Leu Thr Phe Glu Gly Lys Pro Leu Glu Asp Gln Leu Pro		
115	120	125
Leu Gly Glu Tyr Gly Leu Lys Pro Leu Ser Thr Val Phe Met Asn Leu		
130	135	140
Arg Leu Arg Gly Gly Gly Thr Glu Pro Gly Gly Arg Ser		
145	150	155

<210> 21

<211> 5095

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (14)..(2593)

<400> 21

agaggctgcg agc atg ggg ccc tgg ggc tgg aaa ttg cgc tgg acc gtc	49
Met Gly Pro Trp Gly Trp Lys Leu Arg Trp Thr Val	
1 5 10	
gcc ttg ctc ctc gcc gcg gcg ggg act gca gtg ggc gac aga tgt gaa	97
Ala Leu Leu Leu Ala Ala Ala Gly Thr Ala Val Gly Asp Arg Cys Glu	
15 20 25	
aga aac gag ttc cag tgc caa gac ggg aaa tgc atc tcc tac aag tgg	145
Arg Asn Glu Phe Gln Cys Gln Asp Gly Lys Cys Ile Ser Tyr Lys Trp	

1241.22

30	35	40	
gtc tgc gat ggc agc gct gag tgc cag gat ggc tct gat gag tcc cag			193
Val Cys Asp Gly Ser Ala Glu Cys Gln Asp Gly Ser Asp Glu Ser Gln			
45	50	55	60
gag acg tgc ttg tct gtc acc tgc aaa tcc ggg gac ttc agc tgt ggg			241
Glu Thr Cys Leu Ser Val Thr Cys Lys Ser Gly Asp Phe Ser Cys Gly			
65	70	75	
ggc cgt gtc aac cgc tgc att cct cag ttc tgg agg tgc gat ggc caa			289
Gly Arg Val Asn Arg Cys Ile Pro Gln Phe Trp Arg Cys Asp Gly Gln			
80	85	90	
gtg gac tgc gac aac ggc tca gac gag caa ggc tgt ccc ccc aag acg			337
Val Asp Cys Asp Asn Gly Ser Asp Glu Gln Gly Cys Pro Pro Lys Thr			
95	100	105	
tgc tcc cag gac gag ttt cgc tgc cac gat ggg aag tgc atc tct cgg			385
Cys Ser Gln Asp Glu Phe Arg Cys His Asp Gly Lys Cys Ile Ser Arg			
110	115	120	
cag ttc gtc tgt gac tca gac cgg gac tgc ttg gac ggc tca gac gag			433
Gln Phe Val Cys Asp Ser Asp Arg Asp Cys Leu Asp Gly Ser Asp Glu			
125	130	135	140
gcc tcc tgc ccg gtg ctc acc tgt ggt ccc gcc agc ttc cag tgc aac			481
Ala Ser Cys Pro Val Leu Thr Cys Gly Pro Ala Ser Phe Gln Cys Asn			
145	150	155	
agc tcc acc tgc atc ccc cag ctg tgg gcc tgc gac aac gac ccc gac			529
Ser Ser Thr Cys Ile Pro Gln Leu Trp Ala Cys Asp Asn Asp Pro Asp			
160	165	170	
tgc gaa gat ggc tcg gat gag tgg ccg cag cgc tgt agg ggt ctt tac			577
Cys Glu Asp Gly Ser Asp Glu Trp Pro Gln Arg Cys Arg Gly Leu Tyr			
175	180	185	
gtg ttc caa ggg gac agt agc ccc tgc tcg gcc ttc gag ttc cac tgc			625
Val Phe Gln Gly Asp Ser Ser Pro Cys Ser Ala Phe Glu Phe His Cys			
190	195	200	
cta agt ggc gag tgc atc cac tcc agc tgg cgc tgt gat ggt ggc ccc			673

Leu	Ser	Gly	Glu	Cys	Ile	His	Ser	Ser	Trp	Arg	Cys	Asp	Gly	Gly	Pro	
205					210					215					220	
gac	tgc	aag	gac	aaa	tct	gac	gag	gaa	aac	tgc	gct	gtg	gcc	acc	tgt	721
Asp	Cys	Lys	Asp	Lys	Ser	Asp	Glu	Glu	Asn	Cys	Ala	Val	Ala	Thr	Cys	
				225					230					235		
cgc	cct	gac	gaa	ttc	cag	tgc	tct	gat	gga	aac	tgc	atc	cat	ggc	agc	769
Arg	Pro	Asp	Glu	Phe	Gln	Cys	Ser	Asp	Gly	Asn	Cys	Ile	His	Gly	Ser	
			240						245				250			
cgg	cag	tgt	gac	cgg	gaa	tat	gac	tgc	aag	gac	atg	agc	gat	gaa	gtt	817
Arg	Gln	Cys	Asp	Arg	Glu	Tyr	Asp	Cys	Lys	Asp	Met	Ser	Asp	Glu	Val	
		255						260				265				
ggc	tgc	gtt	aat	gtg	aca	ctc	tgc	gag	gga	ccc	aac	aag	ttc	aag	tgt	865
Gly	Cys	Val	Asn	Val	Thr	Leu	Cys	Glu	Gly	Pro	Asn	Lys	Phe	Lys	Cys	
	270					275					280					
cac	agc	ggc	gaa	tgc	atc	acc	ctg	gac	aaa	gtc	tgc	aac	atg	gct	aga	913
His	Ser	Gly	Glu	Cys	Ile	Thr	Leu	Asp	Lys	Val	Cys	Asn	Met	Ala	Arg	
285					290					295					300	
gac	tgc	cgg	gac	tgg	tca	gat	gaa	ccc	atc	aaa	gag	tgc	ggg	acc	aac	961
Asp	Cys	Arg	Asp	Trp	Ser	Asp	Glu	Pro	Ile	Lys	Glu	Cys	Gly	Thr	Asn	
			305						310					315		
gaa	tgc	ttg	gac	aac	aac	ggc	ggc	tgt	tcc	cac	gtc	tgc	aat	gac	ctt	1009
Glu	Cys	Leu	Asp	Asn	Asn	Gly	Gly	Cys	Ser	His	Val	Cys	Asn	Asp	Leu	
			320					325					330			
aag	atc	ggc	tac	gag	tgc	ctg	tgc	ccc	gac	ggc	ttc	cag	ctg	gtg	gcc	1057
Lys	Ile	Gly	Tyr	Glu	Cys	Leu	Cys	Pro	Asp	Gly	Phe	Gln	Leu	Val	Ala	
		335						340				345				
cag	cga	aga	tgc	gaa	gat	atc	gat	gag	tgt	cag	gat	ccc	gac	acc	tgc	1105
Gln	Arg	Arg	Cys	Glu	Asp	Ile	Asp	Glu	Cys	Gln	Asp	Pro	Asp	Thr	Cys	
	350					355					360					
agc	cag	ctc	tgc	gtg	aac	ctg	gag	ggt	ggc	tac	aag	tgc	cag	tgt	gag	1153
Ser	Gln	Leu	Cys	Val	Asn	Leu	Glu	Gly	Gly	Tyr	Lys	Cys	Gln	Cys	Glu	

365		1241.22	
	370	375	380
gaa ggc ttc cag ctg gac ccc cac acg aag gcc tgc aag gct gtg ggc			1201
Glu Gly Phe Gln Leu Asp Pro His Thr Lys Ala Cys Lys Ala Val Gly			
	385	390	395
tcc atc gcc tac ctc ttc ttc acc aac cgg cac gag gtc agg aag atg			1249
Ser Ile Ala Tyr Leu Phe Phe Thr Asn Arg His Glu Val Arg Lys Met			
	400	405	410
acg ctg gac cgg agc gag tac acc agc ctc atc ccc aac ctg agg aac			1297
Thr Leu Asp Arg Ser Glu Tyr Thr Ser Leu Ile Pro Asn Leu Arg Asn			
	415	420	425
gtg gtc gct ctg gac acg gag gtg gcc agc aat aga atc tac tgg tct			1345
Val Val Ala Leu Asp Thr Glu Val Ala Ser Asn Arg Ile Tyr Trp Ser			
	430	435	440
gac ctg tcc cag aga atg atc tgc agc acc cag ctt gac aga gcc cac			1393
Asp Leu Ser Gln Arg Met Ile Cys Ser Thr Gln Leu Asp Arg Ala His			
	445	450	455
ggc gtc tct tcc tat gac acc gtc atc agc agg gac atc cag gcc ccc			1441
Gly Val Ser Ser Tyr Asp Thr Val Ile Ser Arg Asp Ile Gln Ala Pro			
	465	470	475
gac ggg ctg gct gtg gac tgg atc cac agc aac atc tac tgg acc gac			1489
Asp Gly Leu Ala Val Asp Trp Ile His Ser Asn Ile Tyr Trp Thr Asp			
	480	485	490
tct gtc ctg ggc act gtc tct gtt gcg gat acc aag ggc gtg aag agg			1537
Ser Val Leu Gly Thr Val Ser Val Ala Asp Thr Lys Gly Val Lys Arg			
	495	500	505
aaa acg tta ttc agg gag aac ggc tcc aag cca agg gcc atc gtg gtg			1585
Lys Thr Leu Phe Arg Glu Asn Gly Ser Lys Pro Arg Ala Ile Val Val			
	510	515	520
gat cct gtt cat ggc ttc atg tac tgg act gac tgg gga act ccc gcc			1633
Asp Pro Val His Gly Phe Met Tyr Trp Thr Asp Trp Gly Thr Pro Ala			
	525	530	535
aag atc aag aaa ggg ggc ctg aat ggt gtg gac atc tac tcg ctg gtg			1681

1241.22

Lys Ile Lys Lys Gly Gly Leu Asn Gly Val Asp Ile Tyr Ser Leu Val	
545 550 555	
act gaa aac att cag tgg ccc aat ggc atc acc cta gat ctc ctc agt	1729
Thr Glu Asn Ile Gln Trp Pro Asn Gly Ile Thr Leu Asp Leu Leu Ser	
560 565 570	
ggc cgc ctc tac tgg gtt gac tcc aaa ctt cac tcc atc tca agc atc	1777
Gly Arg Leu Tyr Trp Val Asp Ser Lys Leu His Ser Ile Ser Ser Ile	
575 580 585	
gat gtc aat ggg ggc aac cgg aag acc atc ttg gag gat gaa aag agg	1825
Asp Val Asn Gly Gly Asn Arg Lys Thr Ile Leu Glu Asp Glu Lys Arg	
590 595 600	
ctg gcc cac ccc ttc tcc ttg gcc gtc ttt gag gac aaa gta ttt tgg	1873
Leu Ala His Pro Phe Ser Leu Ala Val Phe Glu Asp Lys Val Phe Trp	
605 610 615 620	
aca gat atc atc aac gaa gcc att ttc agt gcc aac cgc ctc aca ggt	1921
Thr Asp Ile Ile Asn Glu Ala Ile Phe Ser Ala Asn Arg Leu Thr Gly	
625 630 635	
tcc gat gtc aac ttg ttg gct gaa aac cta ctg tcc cca gag gat atg	1969
Ser Asp Val Asn Leu Leu Ala Glu Asn Leu Leu Ser Pro Glu Asp Met	
640 645 650	
gtc ctc ttc cac aac ctc acc cag cca aga gga gtg aac tgg tgt gag	2017
Val Leu Phe His Asn Leu Thr Gln Pro Arg Gly Val Asn Trp Cys Glu	
655 660 665	
agg acc acc ctg agc aat ggc ggc tgc cag tat ctg tgc ctc cct gcc	2065
Arg Thr Thr Leu Ser Asn Gly Gly Cys Gln Tyr Leu Cys Leu Pro Ala	
670 675 680	
ccg cag atc aac ccc cac tcg ccc aag ttt acc tgc gcc tgc ccg gac	2113
Pro Gln Ile Asn Pro His Ser Pro Lys Phe Thr Cys Ala Cys Pro Asp	
685 690 695 700	
ggc atg ctg ctg gcc agg gac atg agg agc tgc ctc aca gag gct gag	2161
Gly Met Leu Leu Ala Arg Asp Met Arg Ser Cys Leu Thr Glu Ala Glu	

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705	710	715	
gct gca gtg gcc acc cag gag aca tcc acc gtc agg cta aag gtc agc			2209
Ala Ala Val Ala Thr Gln Glu Thr Ser Thr Val Arg Leu Lys Val Ser			
720	725	730	
tcc aca gcc gta agg aca cag cac aca acc acc cgg cct gtt ccc gac			2257
Ser Thr Ala Val Arg Thr Gln His Thr Thr Thr Arg Pro Val Pro Asp			
735	740	745	
acc tcc cgg ctg cct ggg gcc acc cct ggg ctc acc acg gtg gag ata			2305
Thr Ser Arg Leu Pro Gly Ala Thr Pro Gly Leu Thr Thr Val Glu Ile			
750	755	760	
gtg aca atg tct cac caa gct ctg ggc gac gtt gct ggc aga gga aat			2353
Val Thr Met Ser His Gln Ala Leu Gly Asp Val Ala Gly Arg Gly Asn			
765	770	775	780
gag aag aag ccc agt agc gtg agg gct ctg tcc att gtc ctc ccc atc			2401
Glu Lys Lys Pro Ser Ser Val Arg Ala Leu Ser Ile Val Leu Pro Ile			
785	790	795	
gtg ctc ctc gtc ttc ctt tgc ctg ggg gtc ttc ctt cta tgg aag aac			2449
Val Leu Leu Val Phe Leu Cys Leu Gly Val Phe Leu Leu Trp Lys Asn			
800	805	810	
tgg cgg ctt aag aac atc aac agc atc aac ttt gac aac ccc gtc tat			2497
Trp Arg Leu Lys Asn Ile Asn Ser Ile Asn Phe Asp Asn Pro Val Tyr			
815	820	825	
cag aag acc aca gag gat gag gtc cac att tgc cac aac cag gac ggc			2545
Gln Lys Thr Thr Glu Asp Glu Val His Ile Cys His Asn Gln Asp Gly			
830	835	840	
tac agc tac ccc tcg aga cag atg gtc agt ctg gag gat gac gtg gcg			2593
Tyr Ser Tyr Pro Ser Arg Gln Met Val Ser Leu Glu Asp Asp Val Ala			
845	850	855	860
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<211> 860

<212> PRT

<213> Homo sapiens

<400> 22

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 Gln Cys Gln Asp Gly Lys Cys Ile Ser Tyr Lys Trp Val Cys Asp Gly
 35 40 45
 Ser Ala Glu Cys Gln Asp Gly Ser Asp Glu Ser Gln Glu Thr Cys Leu
 50 55 60
 Ser Val Thr Cys Lys Ser Gly Asp Phe Ser Cys Gly Gly Arg Val Asn
 65 70 75 80
 Arg Cys Ile Pro Gln Phe Trp Arg Cys Asp Gly Gln Val Asp Cys Asp
 85 90 95
 Asn Gly Ser Asp Glu Gln Gly Cys Pro Pro Lys Thr Cys Ser Gln Asp
 100 105 110
 Glu Phe Arg Cys His Asp Gly Lys Cys Ile Ser Arg Gln Phe Val Cys
 115 120 125
 Asp Ser Asp Arg Asp Cys Leu Asp Gly Ser Asp Glu Ala Ser Cys Pro
 130 135 140
 Val Leu Thr Cys Gly Pro Ala Ser Phe Gln Cys Asn Ser Ser Thr Cys

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145	150	155		160
Ile	Pro	Gln	Leu	Trp
Ala	Cys	Asp	Asn	Asp
Pro	Asp	Cys	Glu	Asp
Gly				
	165	170		175
Ser	Asp	Glu	Trp	Pro
Gln	Arg	Cys	Arg	Gly
Leu	Tyr	Val	Phe	Gln
Gly				
	180	185		190
Asp	Ser	Ser	Pro	Cys
Ser	Ala	Phe	Glu	Phe
His	Cys	Leu	Ser	Gly
Glu				
	195	200		205
Cys	Ile	His	Ser	Ser
Trp	Arg	Cys	Asp	Gly
Gly	Pro	Asp	Cys	Lys
Asp				
	210	215		220
Lys	Ser	Asp	Glu	Glu
Asn	Cys	Ala	Val	Ala
Thr	Cys	Arg	Pro	Asp
Glu				
	225	230		235
Phe	Gln	Cys	Ser	Asp
Gly	Asn	Cys	Ile	His
Gly	Ser	Arg	Gln	Cys
Asp				
	245	250		255
Arg	Glu	Tyr	Asp	Cys
Lys	Asp	Met	Ser	Asp
Glu	Val	Gly	Cys	Val
Asn				
	260	265		270
Val	Thr	Leu	Cys	Glu
Gly	Pro	Asn	Lys	Phe
Lys	Cys	His	Ser	Gly
Glu				
	275	280		285
Cys	Ile	Thr	Leu	Asp
Lys	Val	Cys	Asn	Met
Ala	Arg	Asp	Cys	Arg
Asp				
	290	295		300
Trp	Ser	Asp	Glu	Pro
Ile	Lys	Glu	Cys	Gly
Thr	Asn	Glu	Cys	Leu
Asp				
	305	310		315
Asn	Asn	Gly	Gly	Cys
Ser	His	Val	Cys	Asn
Asp	Leu	Lys	Ile	Gly
Tyr				
	325	330		335
Glu	Cys	Leu	Cys	Pro
Asp	Gly	Phe	Gln	Leu
Val	Ala	Gln	Arg	Arg
Cys				
	340	345		350
Glu	Asp	Ile	Asp	Glu
Cys	Gln	Asp	Pro	Asp
Thr	Cys	Ser	Gln	Leu
Cys				
	355	360		365
Val	Asn	Leu	Glu	Gly
Gly	Tyr	Lys	Cys	Gln
Cys	Glu	Glu	Gly	Phe
Gln				
	370	375		380
Leu	Asp	Pro	His	Thr
Lys	Ala	Cys	Lys	Ala
Val	Gly	Ser	Ile	Ala
Tyr				
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Leu	Phe	Phe	Thr	Asn
Arg	His	Glu	Val	Arg
Lys	Met	Thr	Leu	Asp
Arg				

1241.22

405	410	415
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420	425	430
Asp Thr Glu Val Ala Ser Asn Arg Ile Tyr Trp Ser Asp Leu Ser Gln		
435	440	445
Arg Met Ile Cys Ser Thr Gln Leu Asp Arg Ala His Gly Val Ser Ser		
450	455	460
Tyr Asp Thr Val Ile Ser Arg Asp Ile Gln Ala Pro Asp Gly Leu Ala		
465	470	475
Val Asp Trp Ile His Ser Asn Ile Tyr Trp Thr Asp Ser Val Leu Gly		480
485	490	495
Thr Val Ser Val Ala Asp Thr Lys Gly Val Lys Arg Lys Thr Leu Phe		
500	505	510
Arg Glu Asn Gly Ser Lys Pro Arg Ala Ile Val Val Asp Pro Val His		
515	520	525
Gly Phe Met Tyr Trp Thr Asp Trp Gly Thr Pro Ala Lys Ile Lys Lys		
530	535	540
Gly Gly Leu Asn Gly Val Asp Ile Tyr Ser Leu Val Thr Glu Asn Ile		
545	550	555
Gln Trp Pro Asn Gly Ile Thr Leu Asp Leu Leu Ser Gly Arg Leu Tyr		560
565	570	575
Trp Val Asp Ser Lys Leu His Ser Ile Ser Ser Ile Asp Val Asn Gly		
580	585	590
Gly Asn Arg Lys Thr Ile Leu Glu Asp Glu Lys Arg Leu Ala His Pro		
595	600	605
Phe Ser Leu Ala Val Phe Glu Asp Lys Val Phe Trp Thr Asp Ile Ile		
610	615	620
Asn Glu Ala Ile Phe Ser Ala Asn Arg Leu Thr Gly Ser Asp Val Asn		
625	630	635
Leu Leu Ala Glu Asn Leu Leu Ser Pro Glu Asp Met Val Leu Phe His		640
645	650	655

1241.22

Asn Leu Thr Gln Pro Arg Gly Val Asn Trp Cys Glu Arg Thr Thr Leu
660 665 670

Ser Asn Gly Gly Cys Gln Tyr Leu Cys Leu Pro Ala Pro Gln Ile Asn
675 680 685

Pro His Ser Pro Lys Phe Thr Cys Ala Cys Pro Asp Gly Met Leu Leu
690 695 700

Ala Arg Asp Met Arg Ser Cys Leu Thr Glu Ala Glu Ala Ala Val Ala
705 710 715 720

Thr Gln Glu Thr Ser Thr Val Arg Leu Lys Val Ser Ser Thr Ala Val
725 730 735

Arg Thr Gln His Thr Thr Thr Arg Pro Val Pro Asp Thr Ser Arg Leu
740 745 750

Pro Gly Ala Thr Pro Gly Leu Thr Thr Val Glu Ile Val Thr Met Ser
755 760 765

His Gln Ala Leu Gly Asp Val Ala Gly Arg Gly Asn Glu Lys Lys Pro
770 775 780

Ser Ser Val Arg Ala Leu Ser Ile Val Leu Pro Ile Val Leu Leu Val
785 790 795 800

Phe Leu Cys Leu Gly Val Phe Leu Leu Trp Lys Asn Trp Arg Leu Lys
805 810 815

Asn Ile Asn Ser Ile Asn Phe Asp Asn Pro Val Tyr Gln Lys Thr Thr
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<210> 23

<211> 1660

<212> DNA

<213> Homo sapiens

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<400> 23

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Leu Leu Leu Ser Ile Ile Val Leu His Val Ala Val Leu Val Leu Leu

5

10

15

ttc gtc tcc acg atc gtc agc caa tgg atc gtg ggc aat gga cac gca 154

Phe Val Ser Thr Ile Val Ser Gln Trp Ile Val Gly Asn Gly His Ala

20

25

30

35

act gat ctc tgg cag aac tgt agc acc tct tcc tca gga aat gtc cac 202

Thr Asp Leu Trp Gln Asn Cys Ser Thr Ser Ser Ser Gly Asn Val His

40

45

50

cac tgt ttc tca tca tca cca aac gaa tgg ctg cag tct gtc cag gcc 250

His Cys Phe Ser Ser Ser Pro Asn Glu Trp Leu Gln Ser Val Gln Ala

55

60

65

acc atg atc ctg tcg atc atc ttc agc att ctg tct ctg ttc ctg ttc 298

Thr Met Ile Leu Ser Ile Ile Phe Ser Ile Leu Ser Leu Phe Leu Phe

70

75

80

ttc tgc caa ctc ttc acc ctc acc aag ggg ggc agg ttt tac atc act 346

Phe Cys Gln Leu Phe Thr Leu Thr Lys Gly Gly Arg Phe Tyr Ile Thr

85

90

95

gga atc ttc caa att ctt gct ggt ctg tgc gtg atg agt gct gcg gcc 394

Gly Ile Phe Gln Ile Leu Ala Gly Leu Cys Val Met Ser Ala Ala Ala

100

105

110

115

atc tac acg gtg agg cac ccg gag tgg cat ctc acc tcg gat tac tcc 442

Ile Tyr Thr Val Arg His Pro Glu Trp His Leu Thr Ser Asp Tyr Ser

120

125

130

tac ggt ttc gcc tac atc ctg gcc tgg gtg gcc ttc ccc ctg gcc ctt 490

Tyr Gly Phe Ala Tyr Ile Leu Ala Trp Val Ala Phe Pro Leu Ala Leu

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Leu Ser Gly Val Ile Tyr Val Ile Leu Arg Lys Arg Glu

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<212> PRT

<213> Homo sapiens

<400> 24

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Val Leu Leu Phe Val Ser Thr Ile Val Ser Gln Trp Ile Val Gly Asn

1241.22

20 25 30
Gly His Ala Thr Asp Leu Trp Gln Asn Cys Ser Thr Ser Ser Ser Gly
35 40 45
Asn Val His His Cys Phe Ser Ser Ser Pro Asn Glu Trp Leu Gln Ser
50 55 60
Val Gln Ala Thr Met Ile Leu Ser Ile Ile Phe Ser Ile Leu Ser Leu
65 70 75 80
Phe Leu Phe Phe Cys Gln Leu Phe Thr Leu Thr Lys Gly Gly Arg Phe
85 90 95
Tyr Ile Thr Gly Ile Phe Gln Ile Leu Ala Gly Leu Cys Val Met Ser
100 105 110
Ala Ala Ala Ile Tyr Thr Val Arg His Pro Glu Trp His Leu Thr Ser
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Asp Tyr Ser Tyr Gly Phe Ala Tyr Ile Leu Ala Trp Val Ala Phe Pro
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<210> 25

<211> 3116

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (36)..(2717)

<400> 25

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Met Ala Trp Arg Cys Pro

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agg atg ggc agg gtc ccg ctg gcc tgg tgc ttg gcg ctg tgc ggc tgg 101

Arg Met Gly Arg Val Pro Leu Ala Trp Cys Leu Ala Leu Cys Gly Trp

10

15

20

1241.22

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Gly Asn Pro Gly Asn Ile Thr Gly Ala Arg Gly Leu Thr Gly Thr Leu	
40 45 50	
cgg tgt cag ctc cag gtt cag gga gag ccc ccc gag gta cat tgg ctt	245
Arg Cys Gln Leu Gln Val Gln Gly Glu Pro Pro Glu Val His Trp Leu	
55 60 65 70	
cgg gat gga cag atc ctg gag ctc gcg gac agc acc cag acc cag gtg	293
Arg Asp Gly Gln Ile Leu Glu Leu Ala Asp Ser Thr Gln Thr Gln Val	
75 80 85	
ccc ctg ggt gag gat gaa cag gat gac tgg ata gtg gtc agc cag ctc	341
Pro Leu Gly Glu Asp Glu Gln Asp Asp Trp Ile Val Val Ser Gln Leu	
90 95 100	
aga atc acc tcc ctg cag ctt tcc gac acg gga cag tac cag tgt ttg	389
Arg Ile Thr Ser Leu Gln Leu Ser Asp Thr Gly Gln Tyr Gln Cys Leu	
105 110 115	
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Val Phe Leu Gly His Gln Thr Phe Val Ser Gln Pro Gly Tyr Val Gly	
120 125 130	
ctg gag ggc ttg cct tac ttc ctg gag gag ccc gaa gac agg act gtg	485
Leu Glu Gly Leu Pro Tyr Phe Leu Glu Glu Pro Glu Asp Arg Thr Val	
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gcc gcc aac acc ccc ttc aac ctg agc tgc caa gct cag gga ccc cca	533
Ala Ala Asn Thr Pro Phe Asn Leu Ser Cys Gln Ala Gln Gly Pro Pro	
155 160 165	
gag ccc gtg gac cta ctc tgg ctc cag gat gct gtc ccc ctg gcc acg	581
Glu Pro Val Asp Leu Leu Trp Leu Gln Asp Ala Val Pro Leu Ala Thr	
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Ala Pro Gly His Gly Pro Gln Arg Ser Leu His Val Pro Gly Leu Asn	
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Lys Thr Ser Ser Phe Ser Cys Glu Ala His Asn Ala Lys Gly Val Thr	
200 205 210	
aca tcc cgc aca gcc acc atc aca gtg ctc ccc cag cag ccc cgt aac	725
Thr Ser Arg Thr Ala Thr Ile Thr Val Leu Pro Gln Gln Pro Arg Asn	
215 220 225 230	
ctc cac ctg gtc tcc cgc caa ccc acg gag ctg gag gtg gct tgg act	773
Leu His Leu Val Ser Arg Gln Pro Thr Glu Leu Glu Val Ala Trp Thr	
235 240 245	
cca ggc ctg agc ggc atc tac ccc ctg acc cac tgc acc ctg cag gct	821
Pro Gly Leu Ser Gly Ile Tyr Pro Leu Thr His Cys Thr Leu Gln Ala	
250 255 260	
gtg ctg tca gac gat ggg atg ggc atc cag gcg gga gaa cca gac ccc	869
Val Leu Ser Asp Asp Gly Met Gly Ile Gln Ala Gly Glu Pro Asp Pro	
265 270 275	
cca gag gag ccc ctc acc tcg caa gca tcc gtg ccc ccc cat cag ctt	917
Pro Glu Glu Pro Leu Thr Ser Gln Ala Ser Val Pro Pro His Gln Leu	
280 285 290	
cgg cta ggc agc ctc cat cct cac ccc cct tat cac atc cgc gtg gca	965
Arg Leu Gly Ser Leu His Pro His Pro Pro Tyr His Ile Arg Val Ala	
295 300 305 310	
tgc acc agc agc cag ggc ccc tca tcc tgg acc cac tgg ctt cct gtg	1013
Cys Thr Ser Ser Gln Gly Pro Ser Ser Trp Thr His Trp Leu Pro Val	
315 320 325	
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Glu Thr Pro Glu Gly Val Pro Leu Gly Pro Pro Glu Asn Ile Ser Ala	
330 335 340	
acg cgg aat ggg agc cag gcc ttc gtg cat tgg caa gag ccc cgg gcg	1109
Thr Arg Asn Gly Ser Gln Ala Phe Val His Trp Gln Glu Pro Arg Ala	
345 350 355	

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gac acc cca gag gtg cta atg gac ata ggg cta agg caa gag gtg acc	1205
Asp Thr Pro Glu Val Leu Met Asp Ile Gly Leu Arg Gln Glu Val Thr	
375 380 385 390	
ctg gag ctg cag ggg gac ggg tct gtg tcc aat ctg aca gtg tgt gtg	1253
Leu Glu Leu Gln Gly Asp Gly Ser Val Ser Asn Leu Thr Val Cys Val	
395 400 405	
gca gcc tac act gct gct ggg gat gga ccc tgg agc ctc cca gta ccc	1301
Ala Ala Tyr Thr Ala Ala Gly Asp Gly Pro Trp Ser Leu Pro Val Pro	
410 415 420	
ctg gag gcc tgg cgc cca ggg gaa gca cag cca gtc cac cag ctg gtg	1349
Leu Glu Ala Trp Arg Pro Gly Glu Ala Gln Pro Val His Gln Leu Val	
425 430 435	
aag gaa cct tca act cct gcc ttc tcg tgg ccc tgg tgg tat gta ctg	1397
Lys Glu Pro Ser Thr Pro Ala Phe Ser Trp Pro Trp Trp Tyr Val Leu	
440 445 450	
cta gga gca gtc gtg gcc gct gcc tgt gtc ctc atc ttg gct ctc ttc	1445
Leu Gly Ala Val Val Ala Ala Ala Cys Val Leu Ile Leu Ala Leu Phe	
455 460 465 470	
ctt gtc cac cgg cga aag aag gag acc cgt tat gga gaa gtg ttt gaa	1493
Leu Val His Arg Arg Lys Lys Glu Thr Arg Tyr Gly Glu Val Phe Glu	
475 480 485	
cca aca gtg gaa aga ggt gaa ctg gta gtc agg tac cgc gtg cgc aag	1541
Pro Thr Val Glu Arg Gly Glu Leu Val Val Arg Tyr Arg Val Arg Lys	
490 495 500	
tcc tac agt cgt cgg acc act gaa gct acc ttg aac agc ctg ggc atc	1589
Ser Tyr Ser Arg Arg Thr Thr Glu Ala Thr Leu Asn Ser Leu Gly Ile	
505 510 515	
agt gaa gag ctg aag gag aag ctg cgg gat gtg atg gtg gac cgg cac	1637

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Ser Glu Glu Leu Lys Glu Lys Leu Arg Asp Val Met Val Asp Arg His	
520 525 530	
aag gtg gcc ctg ggg aag act ctg gga gag gga gag ttt gga gct gtg	1685
Lys Val Ala Leu Gly Lys Thr Leu Gly Glu Gly Glu Phe Gly Ala Val	
535 540 545 550	
atg gaa ggc cag ctc aac cag gac gac tcc atc ctc aag gtg gct gtg	1733
Met Glu Gly Gln Leu Asn Gln Asp Asp Ser Ile Leu Lys Val Ala Val	
555 560 565	
aag acg atg aag att gcc atc tgc acg agg tca gag ctg gag gat ttc	1781
Lys Thr Met Lys Ile Ala Ile Cys Thr Arg Ser Glu Leu Glu Asp Phe	
570 575 580	
ctg agt gaa gcg gtc tgc atg aag gaa ttt gac cat ccc aac gtc atg	1829
Leu Ser Glu Ala Val Cys Met Lys Glu Phe Asp His Pro Asn Val Met	
585 590 595	
agg ctc atc ggt gtc tgt ttc cag ggt tct gaa cga gag agc ttc cca	1877
Arg Leu Ile Gly Val Cys Phe Gln Gly Ser Glu Arg Glu Ser Phe Pro	
600 605 610	
gca cct gtg gtc atc tta cct ttc atg aaa cat gga gac cta cac agc	1925
Ala Pro Val Val Ile Leu Pro Phe Met Lys His Gly Asp Leu His Ser	
615 620 625 630	
ttc ctc ctc tat tcc cgg ctc ggg ggc cag cca gtg tac ctg ccc act	1973
Phe Leu Leu Tyr Ser Arg Leu Gly Gly Gln Pro Val Tyr Leu Pro Thr	
635 640 645	
cag atg cta gtg aag ttc atg gca gac atc gcc agt ggc atg gag tat	2021
Gln Met Leu Val Lys Phe Met Ala Asp Ile Ala Ser Gly Met Glu Tyr	
650 655 660	
ctg agt acc aag aga ttc ata cac cgg gac ctg gcg gcc agg aac tgc	2069
Leu Ser Thr Lys Arg Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys	
665 670 675	
atg ctg aat gag aac atg tcc gtg tgt gtg gcg gac ttc ggg ctc tcc	2117
Met Leu Asn Glu Asn Met Ser Val Cys Val Ala Asp Phe Gly Leu Ser	
680 685 690	

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Lys Lys Ile Tyr Asn Gly Asp Tyr Tyr Arg Gln Gly Arg Ile Ala Lys	
695 700 705 710	
atg cca gtc aag tgg att gcc att gag agt cta gct gac cgt gtc tac	2213
Met Pro Val Lys Trp Ile Ala Ile Glu Ser Leu Ala Asp Arg Val Tyr	
715 720 725	
acc agc aag agc gat gtg tgg tcc ttc ggg gtg aca atg tgg gag att	2261
Thr Ser Lys Ser Asp Val Trp Ser Phe Gly Val Thr Met Trp Glu Ile	
730 735 740	
gcc aca aga ggc caa acc cca tat ccg ggc gtg gag aac agc gag att	2309
Ala Thr Arg Gly Gln Thr Pro Tyr Pro Gly Val Glu Asn Ser Glu Ile	
745 750 755	
tat gac tat ctg cgc cag gga aat cgc ctg aag cag cct gcg gac tgt	2357
Tyr Asp Tyr Leu Arg Gln Gly Asn Arg Leu Lys Gln Pro Ala Asp Cys	
760 765 770	
ctg gat gga ctg tat gcc ttg atg tcg cgg tgc tgg gag cta aat ccc	2405
Leu Asp Gly Leu Tyr Ala Leu Met Ser Arg Cys Trp Glu Leu Asn Pro	
775 780 785 790	
cag gac cgg cca agt ttt aca gag ctg cgg gaa gat ttg gag aac aca	2453
Gln Asp Arg Pro Ser Phe Thr Glu Leu Arg Glu Asp Leu Glu Asn Thr	
795 800 805	
ctg aag gcc ttg cct cct gcc cag gag cct gac gaa atc ctc tat gtc	2501
Leu Lys Ala Leu Pro Pro Ala Gln Glu Pro Asp Glu Ile Leu Tyr Val	
810 815 820	
aac atg gat gag ggt gga ggt tat cct gaa ccc cct gga gct gca gga	2549
Asn Met Asp Glu Gly Gly Gly Tyr Pro Glu Pro Pro Gly Ala Ala Gly	
825 830 835	
gga gct gac ccc cca acc cag cca gac cct aag gat tcc tgt agc tgc	2597
Gly Ala Asp Pro Pro Thr Gln Pro Asp Pro Lys Asp Ser Cys Ser Cys	
840 845 850	
ctc act gcg gct gag gtc cat cct gct gga cgc tat gtc ctc tgc cct	2645

1241.22

Leu Thr Ala Ala Glu Val His Pro Ala Gly Arg Tyr Val Leu Cys Pro
 855 860 865 870
 tcc aca acc cct agc ccc gct cag cct gct gat agg ggc tcc cca gca 2693
 Ser Thr Thr Pro Ser Pro Ala Gln Pro Ala Asp Arg Gly Ser Pro Ala
 875 880 885
 gcc cca ggg cag gag gat ggt gcc tgagacaacc ctccacctgg tactccctct 2747
 Ala Pro Gly Gln Glu Asp Gly Ala

890

caggatccaa gctaagcact gccactgggg gaaactccac cttcccactt tcccacccca 2807
 cgccttatcc ccacttgtag cctgtcttc ctacctatcc cacctccatc ccagacaggt 2867
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 ggcctaaaa 3116

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<211> 894

<212> PRT

<213> Homo sapiens

<400> 26

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 20 25 30
 Glu Glu Ser Pro Phe Val Gly Asn Pro Gly Asn Ile Thr Gly Ala Arg
 35 40 45
 Gly Leu Thr Gly Thr Leu Arg Cys Gln Leu Gln Val Gln Gly Glu Pro
 50 55 60
 Pro Glu Val His Trp Leu Arg Asp Gly Gln Ile Leu Glu Leu Ala Asp
 65 70 75 80
 Ser Thr Gln Thr Gln Val Pro Leu Gly Glu Asp Glu Gln Asp Asp Trp

1241.22

85	90	95
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Gly Gln Tyr Gln Cys Leu Val Phe Leu Gly His Gln Thr Phe Val Ser		
115	120	125
Gln Pro Gly Tyr Val Gly Leu Glu Gly Leu Pro Tyr Phe Leu Glu Glu		
130	135	140
Pro Glu Asp Arg Thr Val Ala Ala Asn Thr Pro Phe Asn Leu Ser Cys		
145	150	155
Gln Ala Gln Gly Pro Pro Glu Pro Val Asp Leu Leu Trp Leu Gln Asp		
165	170	175
Ala Val Pro Leu Ala Thr Ala Pro Gly His Gly Pro Gln Arg Ser Leu		
180	185	190
His Val Pro Gly Leu Asn Lys Thr Ser Ser Phe Ser Cys Glu Ala His		
195	200	205
Asn Ala Lys Gly Val Thr Thr Ser Arg Thr Ala Thr Ile Thr Val Leu		
210	215	220
Pro Gln Gln Pro Arg Asn Leu His Leu Val Ser Arg Gln Pro Thr Glu		
225	230	235
Leu Glu Val Ala Trp Thr Pro Gly Leu Ser Gly Ile Tyr Pro Leu Thr		
245	250	255
His Cys Thr Leu Gln Ala Val Leu Ser Asp Asp Gly Met Gly Ile Gln		
260	265	270
Ala Gly Glu Pro Asp Pro Pro Glu Glu Pro Leu Thr Ser Gln Ala Ser		
275	280	285
Val Pro Pro His Gln Leu Arg Leu Gly Ser Leu His Pro His Pro Pro		
290	295	300
Tyr His Ile Arg Val Ala Cys Thr Ser Ser Gln Gly Pro Ser Ser Trp		
305	310	315
Thr His Trp Leu Pro Val Glu Thr Pro Glu Gly Val Pro Leu Gly Pro		
325	330	335
Pro Glu Asn Ile Ser Ala Thr Arg Asn Gly Ser Gln Ala Phe Val His		

1241.22

340	345	350	
Trp Gln Glu Pro Arg Ala Pro Leu Gln Gly Thr Leu Leu Gly Tyr Arg			
355	360	365	
Leu Ala Tyr Gln Gly Gln Asp Thr Pro Glu Val Leu Met Asp Ile Gly			
370	375	380	
Leu Arg Gln Glu Val Thr Leu Glu Leu Gln Gly Asp Gly Ser Val Ser			
385	390	395	400
Asn Leu Thr Val Cys Val Ala Ala Tyr Thr Ala Ala Gly Asp Gly Pro			
405	410	415	
Trp Ser Leu Pro Val Pro Leu Glu Ala Trp Arg Pro Gly Glu Ala Gln			
420	425	430	
Pro Val His Gln Leu Val Lys Glu Pro Ser Thr Pro Ala Phe Ser Trp			
435	440	445	
Pro Trp Trp Tyr Val Leu Leu Gly Ala Val Val Ala Ala Ala Cys Val			
450	455	460	
Leu Ile Leu Ala Leu Phe Leu Val His Arg Arg Lys Lys Glu Thr Arg			
465	470	475	480
Tyr Gly Glu Val Phe Glu Pro Thr Val Glu Arg Gly Glu Leu Val Val			
485	490	495	
Arg Tyr Arg Val Arg Lys Ser Tyr Ser Arg Arg Thr Thr Glu Ala Thr			
500	505	510	
Leu Asn Ser Leu Gly Ile Ser Glu Glu Leu Lys Glu Lys Leu Arg Asp			
515	520	525	
Val Met Val Asp Arg His Lys Val Ala Leu Gly Lys Thr Leu Gly Glu			
530	535	540	
Gly Glu Phe Gly Ala Val Met Glu Gly Gln Leu Asn Gln Asp Asp Ser			
545	550	555	560
Ile Leu Lys Val Ala Val Lys Thr Met Lys Ile Ala Ile Cys Thr Arg			
565	570	575	
Ser Glu Leu Glu Asp Phe Leu Ser Glu Ala Val Cys Met Lys Glu Phe			
580	585	590	

1241.22

Asp His Pro Asn Val Met Arg Leu Ile Gly Val Cys Phe Gln Gly Ser
595 600 605

Glu Arg Glu Ser Phe Pro Ala Pro Val Val Ile Leu Pro Phe Met Lys
610 615 620

His Gly Asp Leu His Ser Phe Leu Leu Tyr Ser Arg Leu Gly Gly Gln
625 630 635 640

Pro Val Tyr Leu Pro Thr Gln Met Leu Val Lys Phe Met Ala Asp Ile
645 650 655

Ala Ser Gly Met Glu Tyr Leu Ser Thr Lys Arg Phe Ile His Arg Asp
660 665 670

Leu Ala Ala Arg Asn Cys Met Leu Asn Glu Asn Met Ser Val Cys Val
675 680 685

Ala Asp Phe Gly Leu Ser Lys Lys Ile Tyr Asn Gly Asp Tyr Tyr Arg
690 695 700

Gln Gly Arg Ile Ala Lys Met Pro Val Lys Trp Ile Ala Ile Glu Ser
705 710 715 720

Leu Ala Asp Arg Val Tyr Thr Ser Lys Ser Asp Val Trp Ser Phe Gly
725 730 735

Val Thr Met Trp Glu Ile Ala Thr Arg Gly Gln Thr Pro Tyr Pro Gly
740 745 750

Val Glu Asn Ser Glu Ile Tyr Asp Tyr Leu Arg Gln Gly Asn Arg Leu
755 760 765

Lys Gln Pro Ala Asp Cys Leu Asp Gly Leu Tyr Ala Leu Met Ser Arg
770 775 780

Cys Trp Glu Leu Asn Pro Gln Asp Arg Pro Ser Phe Thr Glu Leu Arg
785 790 795 800

Glu Asp Leu Glu Asn Thr Leu Lys Ala Leu Pro Pro Ala Gln Glu Pro
805 810 815

Asp Glu Ile Leu Tyr Val Asn Met Asp Glu Gly Gly Gly Tyr Pro Glu
820 825 830

Pro Pro Gly Ala Ala Gly Gly Ala Asp Pro Pro Thr Gln Pro Asp Pro
835 840 845

1241.22

Lys Asp Ser Cys Ser Cys Leu Thr Ala Ala Glu Val His Pro Ala Gly
850 855 860
Arg Tyr Val Leu Cys Pro Ser Thr Thr Pro Ser Pro Ala Gln Pro Ala
865 870 875 880
Asp Arg Gly Ser Pro Ala Ala Pro Gly Gln Glu Asp Gly Ala
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<212> DNA

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Phe Gly Val Asn Glu Ser Thr Gly Leu Ser Leu Glu Gln Val Lys Lys
20 25 30
ctt aag gag aga tgg ggc tcc aac gag tta ccg gct gaa gaa gga aaa 144
Leu Lys Glu Arg Trp Gly Ser Asn Glu Leu Pro Ala Glu Glu Gly Lys
35 40 45
acc ttg ctg gaa ctt gtg att gag cag ttt gaa gac ttg cta gtt agg 192
Thr Leu Leu Glu Leu Val Ile Glu Gln Phe Glu Asp Leu Leu Val Arg
50 55 60
att tta tta ctg gca gca tgt ata tct ttt gtt ttg gct tgg ttt gaa 240
Ile Leu Leu Leu Ala Ala Cys Ile Ser Phe Val Leu Ala Trp Phe Glu
65 70 75
gaa ggt gaa gaa aca att aca gcc ttt gta gaa cct ttt gta att tta 288
Glu Gly Glu Glu Thr Ile Thr Ala Phe Val Glu Pro Phe Val Ile Leu
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80	85	90	95	
ctc ata tta gta gcc aat gca att gtg ggt gta tgg cag gaa aga aat	336			
Leu Ile Leu Val Ala Asn Ala Ile Val Gly Val Trp Gln Glu Arg Asn				
100	105	110		
gct gaa aat gcc atc gaa gcc ctt aag gaa tat gag cct gaa atg ggc	384			
Ala Glu Asn Ala Ile Glu Ala Leu Lys Glu Tyr Glu Pro Glu Met Gly				
115	120	125		
aaa gtg tat cga cag gac aga aag agt gtg cag cgg att aaa gct aaa	432			
Lys Val Tyr Arg Gln Asp Arg Lys Ser Val Gln Arg Ile Lys Ala Lys				
130	135	140		
gac ata gtt cct ggt gat att gta gaa att gct gtt ggt gac aaa gtt	480			
Asp Ile Val Pro Gly Asp Ile Val Glu Ile Ala Val Gly Asp Lys Val				
145	150	155		
cct gct gat ata agg tta act tcc atc aaa tct acc aca cta aga gtt	528			
Pro Ala Asp Ile Arg Leu Thr Ser Ile Lys Ser Thr Thr Leu Arg Val				
160	165	170	175	
gac cag tca att ctc aca ggt gaa tct gtc tct gtc atc aag cac act	576			
Asp Gln Ser Ile Leu Thr Gly Glu Ser Val Ser Val Ile Lys His Thr				
180	185	190		
gat ccc gtc cct gac cca cga gct gtc aac caa gat aaa aag aac atg	624			
Asp Pro Val Pro Asp Pro Arg Ala Val Asn Gln Asp Lys Lys Asn Met				
195	200	205		
ctg ttt tct ggt aca aac att gct gct ggg aaa gct atg gga gtg gtg	672			
Leu Phe Ser Gly Thr Asn Ile Ala Ala Gly Lys Ala Met Gly Val Val				
210	215	220		
gta gca act gga gtt aac acc gaa att ggc aag atc cgg gat gaa atg	720			
Val Ala Thr Gly Val Asn Thr Glu Ile Gly Lys Ile Arg Asp Glu Met				
225	230	235		
gtg gca aca gaa cag gag aga aca ccc ctt cag caa aaa cta gat gaa	768			
Val Ala Thr Glu Gln Glu Arg Thr Pro Leu Gln Gln Lys Leu Asp Glu				
240	245	250	255	

1241.22

ttt ggg gaa cag ctt tcc aaa gtc atc tcc ctt att tgc att gca gtc	816
Phe Gly Glu Gln Leu Ser Lys Val Ile Ser Leu Ile Cys Ile Ala Val	
260 265 270	
tgg atc ata aat att ggg cac ttc aat gac ccg gtt cat gga ggg tcc	864
Trp Ile Ile Asn Ile Gly His Phe Asn Asp Pro Val His Gly Gly Ser	
275 280 285	
tgg atc aga ggt gct att tac tac ttt aaa att gca gtg gcc ctg gct	912
Trp Ile Arg Gly Ala Ile Tyr Tyr Phe Lys Ile Ala Val Ala Leu Ala	
290 295 300	
gta gca gcc att cct gaa ggt ctg cct gca gtc atc acc acc tgc ctg	960
Val Ala Ala Ile Pro Glu Gly Leu Pro Ala Val Ile Thr Thr Cys Leu	
305 310 315	
gct ctt gga act cgc aga atg gca aag aaa aat gcc att gtt cga agc	1008
Ala Leu Gly Thr Arg Arg Met Ala Lys Lys Asn Ala Ile Val Arg Ser	
320 325 330 335	
ctc ccg tct gtg gaa acc ctt ggt tgt act tct gtt atc tgc tca gac	1056
Leu Pro Ser Val Glu Thr Leu Gly Cys Thr Ser Val Ile Cys Ser Asp	
340 345 350	
aag act ggt aca ctt aca aca aac cag atg tca gtc tgc agg atg ttc	1104
Lys Thr Gly Thr Leu Thr Thr Asn Gln Met Ser Val Cys Arg Met Phe	
355 360 365	
att ctg gac aga gtg gaa ggt gat act tgt tcc ctt aat gag ttt acc	1152
Ile Leu Asp Arg Val Glu Gly Asp Thr Cys Ser Leu Asn Glu Phe Thr	
370 375 380	
ata act gga tca act tat gca cct att gga gaa gtg cat aaa gat gat	1200
Ile Thr Gly Ser Thr Tyr Ala Pro Ile Gly Glu Val His Lys Asp Asp	
385 390 395	
aaa cca gtg aat tgt cac cag tat gat ggt ctg gta gaa tta gca aca	1248
Lys Pro Val Asn Cys His Gln Tyr Asp Gly Leu Val Glu Leu Ala Thr	
400 405 410 415	
att tgt gct ctt tgt aat gac tct gct ttg gat tac aat gag gca aag	1296
Ile Cys Ala Leu Cys Asn Asp Ser Ala Leu Asp Tyr Asn Glu Ala Lys	

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420	425	430	
ggt gtg tat gaa aaa gtt gga gaa gct aca gag act gct ctc act tgc			1344
Gly Val Tyr Glu Lys Val Gly Glu Ala Thr Glu Thr Ala Leu Thr Cys			
435	440	445	
cta gta gag aag atg aat gta ttt gat acc gaa ttg aag ggt ctt tct			1392
Leu Val Glu Lys Met Asn Val Phe Asp Thr Glu Leu Lys Gly Leu Ser			
450	455	460	
aaa ata gaa cgt gca aat gcc tgc aac tca gtc att aaa cag ctg atg			1440
Lys Ile Glu Arg Ala Asn Ala Cys Asn Ser Val Ile Lys Gln Leu Met			
465	470	475	
aaa aag gaa ttc act cta gag ttt tca cgt gac aga aag tca atg tcg			1488
Lys Lys Glu Phe Thr Leu Glu Phe Ser Arg Asp Arg Lys Ser Met Ser			
480	485	490	495
gtt tac tgt aca cca aat aaa cca agc agg aca tca atg agc aag atg			1536
Val Tyr Cys Thr Pro Asn Lys Pro Ser Arg Thr Ser Met Ser Lys Met			
500	505	510	
ttt gtg aag ggt gct cct gaa ggt gtc att gac agg tgc acc cac att			1584
Phe Val Lys Gly Ala Pro Glu Gly Val Ile Asp Arg Cys Thr His Ile			
515	520	525	
cga gtt gga agt act aag gtt cct atg acc tct gga gtc aaa cag aag			1632
Arg Val Gly Ser Thr Lys Val Pro Met Thr Ser Gly Val Lys Gln Lys			
530	535	540	
atc atg tct gtc att cga gag tgg ggt agt ggc agc gac aca ctg cga			1680
Ile Met Ser Val Ile Arg Glu Trp Gly Ser Gly Ser Asp Thr Leu Arg			
545	550	555	
tgc ctg gcc ctg gcc act cat gac aac cca ctg aga aga gaa gaa atg			1728
Cys Leu Ala Leu Ala Thr His Asp Asn Pro Leu Arg Arg Glu Glu Met			
560	565	570	575
cac ctt gag gac tct gcc aac ttt att aaa tat gag acc aat ctg acc			1776
His Leu Glu Asp Ser Ala Asn Phe Ile Lys Tyr Glu Thr Asn Leu Thr			
580	585	590	

1241.22

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Phe Val Gly Cys Val Gly Met Leu Asp Pro Pro Arg Ile Glu Val Ala	
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Ser Ser Val Lys Leu Cys Arg Gln Ala Gly Ile Arg Val Ile Met Ile	
610 615 620	
act ggg gac aac aag ggc act gct gtg gcc atc tgt cgc cgc atc ggc	1920
Thr Gly Asp Asn Lys Gly Thr Ala Val Ala Ile Cys Arg Arg Ile Gly	
625 630 635	
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Ile Phe Gly Gln Asp Glu Asp Val Thr Ser Lys Ala Phe Thr Gly Arg	
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Glu Phe Asp Glu Leu Asn Pro Ser Ala Gln Arg Asp Ala Cys Leu Asn	
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gcc cgc tgt ttt gct cga gtt gaa ccc tcc cac aag tct aaa atc gta	2064
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675 680 685	
gaa ttt ctt cag tct ttt gat gag att aca gct atg act ggc gat ggc	2112
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690 695 700	
gtg aac gat gct cct gct ctg aag aaa gcc gag att ggc att gct atg	2160
Val Asn Asp Ala Pro Ala Leu Lys Lys Ala Glu Ile Gly Ile Ala Met	
705 710 715	
ggc tct ggc act gcg gtg gct aaa acc gcc tct gag atg gtc ctg gcg	2208
Gly Ser Gly Thr Ala Val Ala Lys Thr Ala Ser Glu Met Val Leu Ala	
720 725 730 735	
gat gac aac ttc tcc acc att gtg gct gcc gtt gag gag ggg cgg gca	2256
Asp Asp Asn Phe Ser Thr Ile Val Ala Ala Val Glu Glu Gly Arg Ala	
740 745 750	
atc tac aac aac atg aaa cag ttc atc cgc tac ctc atc tcg tcc aac	2304
Ile Tyr Asn Asn Met Lys Gln Phe Ile Arg Tyr Leu Ile Ser Ser Asn	

1241.22

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770	775	780	
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Glu Ala Leu Ile Pro Val Gln Leu Leu Trp Val Asn Leu Val Thr Asp			
785	790	795	
ggc ctg cct gcc act gca ctg ggg ttc aac cct cct gat ctg gac atc			2448
Gly Leu Pro Ala Thr Ala Leu Gly Phe Asn Pro Pro Asp Leu Asp Ile			
800	805	810	815
atg aat aaa cct ccc cgg aac cca aag gaa cca ttg atc agc ggg tgg			2496
Met Asn Lys Pro Pro Arg Asn Pro Lys Glu Pro Leu Ile Ser Gly Trp			
820	825	830	
ctc ttt ttc cgt tac ttg gct att ggc tgt tac gtc ggc gct gct acc			2544
Leu Phe Phe Arg Tyr Leu Ala Ile Gly Cys Tyr Val Gly Ala Ala Thr			
835	840	845	
gtg ggt gct gct gca tgg tgg ttc att gct gct gac ggt ggt cca aga			2592
val Gly Ala Ala Ala Trp Trp Phe Ile Ala Ala Asp Gly Gly Pro Arg			
850	855	860	
gtg tcc ttc tac cag ctg agt cat ttc cta cag tgt aaa gag gac aac			2640
Val Ser Phe Tyr Gln Leu Ser His Phe Leu Gln Cys Lys Glu Asp Asn			
865	870	875	
ccg gac ttt gaa ggc gtg gat tgt gca atc ttt gaa tcc cca tac ccg			2688
Pro Asp Phe Glu Gly Val Asp Cys Ala Ile Phe Glu Ser Pro Tyr Pro			
880	885	890	895
atg aca atg gcg ctc tct gtt cta gta act ata gaa atg tgt aac gcc			2736
Met Thr Met Ala Leu Ser Val Leu Val Thr Ile Glu Met Cys Asn Ala			
900	905	910	
ctc aac agc ttg tcc gaa aac cag tcc ttg ctg agg atg ccc ccc tgg			2784
Leu Asn Ser Leu Ser Glu Asn Gln Ser Leu Leu Arg Met Pro Pro Trp			
915	920	925	

1241.22

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 Glu Asn Ile Trp Leu Val Gly Ser Ile Cys Leu Ser Met Ser Leu His

930 935 940

ttc ctg atc ctc tat gtc gaa ccc ttg cca ctc atc ttc cag atc aca 2880
 Phe Leu Ile Leu Tyr Val Glu Pro Leu Pro Leu Ile Phe Gln Ile Thr

945 950 955

ccg ctg aac gtg acc cag tgg ctg atg gtg ctg aaa atc tcc ttg ccc 2928
 Pro Leu Asn Val Thr Gln Trp Leu Met Val Leu Lys Ile Ser Leu Pro

960 965 970 975

gtg att ctc atg gat gag acg ctc aag ttt gtg gcc cgc aac tac ctg 2976
 Val Ile Leu Met Asp Glu Thr Leu Lys Phe Val Ala Arg Asn Tyr Leu

980 985 990

gaa cct gca ata ctg gag taaccgcttc ctaaaccatt ttgcagaaat 3024
 Glu Pro Ala Ile Leu Glu

995

gtaagggtgt tcggttgctg gcatgtgcgt ttttagcaac acatctacca accctgtgca 3084
 tgactgatgt tggggaaaaa gaaaagtaaa aaacttccca actcactttg tgttatgtgg 3144
 aggaaatgtg tattaccaat ggggttggtta gcttttaaat caaaatactg attacagatg 3204
 tacaatttag cttaatcaga aagcctctcc agagaagttt ggtttctttg ctgcaagagg 3264
 aatgaggctc tgtaacctta tctaagaact tggaagccgt cagccaagtc gccacatttc 3324
 tctgcaaaat gtcatagctt atataaatgt acagtattca attgtaatgc atgcttcggt 3384
 tgtaagtagc cagatccctc tccagtgaca ttggaacatg ctacttttta attggccctg 3444
 tacagtttgc ttatttataa attcattaaa aacactacag gtgttgaaatg gttaaaatgt 3504
 aggccctcag ttcattttca gttattttct gagtgtgcag acagctattt cgcactgtat 3564
 taaatgtaac ttatttaatg aaatcagaag cagtagacag atgttggtgc aatacaata 3624
 ttgtgatgca tttatcttaa taaaatgcta aatgtcaatt tatcactgcg catgtttgac 3684
 tttagactgt aaatagagat cagtttggtt ctttctgtgc tggtacaat gagcgtcgca 3744
 cagacatggt ttcaggtaaa taaatctatt ctatgat 3781

<210> 28

<211> 997

<212> PRT

1241.22

<213> Homo sapiens

<400> 28

Met Glu Asn Ala His Thr Lys Thr Val Glu Glu Val Leu Gly His Phe

1 5 10 15

Gly Val Asn Glu Ser Thr Gly Leu Ser Leu Glu Gln Val Lys Lys Leu

20 25 30

Lys Glu Arg Trp Gly Ser Asn Glu Leu Pro Ala Glu Glu Gly Lys Thr

35 40 45

Leu Leu Glu Leu Val Ile Glu Gln Phe Glu Asp Leu Leu Val Arg Ile

50 55 60

Leu Leu Leu Ala Ala Cys Ile Ser Phe Val Leu Ala Trp Phe Glu Glu

65 70 75 80

Gly Glu Glu Thr Ile Thr Ala Phe Val Glu Pro Phe Val Ile Leu Leu

85 90 95

Ile Leu Val Ala Asn Ala Ile Val Gly Val Trp Gln Glu Arg Asn Ala

100 105 110

Glu Asn Ala Ile Glu Ala Leu Lys Glu Tyr Glu Pro Glu Met Gly Lys

115 120 125

Val Tyr Arg Gln Asp Arg Lys Ser Val Gln Arg Ile Lys Ala Lys Asp

130 135 140

Ile Val Pro Gly Asp Ile Val Glu Ile Ala Val Gly Asp Lys Val Pro

145 150 155 160

Ala Asp Ile Arg Leu Thr Ser Ile Lys Ser Thr Thr Leu Arg Val Asp

165 170 175

Gln Ser Ile Leu Thr Gly Glu Ser Val Ser Val Ile Lys His Thr Asp

180 185 190

Pro Val Pro Asp Pro Arg Ala Val Asn Gln Asp Lys Lys Asn Met Leu

195 200 205

Phe Ser Gly Thr Asn Ile Ala Ala Gly Lys Ala Met Gly Val Val Val

210 215 220

Ala Thr Gly Val Asn Thr Glu Ile Gly Lys Ile Arg Asp Glu Met Val

225 230 235 240

1241.22

Ala Thr Glu Gln Glu Arg Thr Pro Leu Gln Gln Lys Leu Asp Glu Phe
245 250 255
Gly Glu Gln Leu Ser Lys Val Ile Ser Leu Ile Cys Ile Ala Val Trp
260 265 270
Ile Ile Asn Ile Gly His Phe Asn Asp Pro Val His Gly Gly Ser Trp
275 280 285
Ile Arg Gly Ala Ile Tyr Tyr Phe Lys Ile Ala Val Ala Leu Ala Val
290 295 300
Ala Ala Ile Pro Glu Gly Leu Pro Ala Val Ile Thr Thr Cys Leu Ala
305 310 315 320
Leu Gly Thr Arg Arg Met Ala Lys Lys Asn Ala Ile Val Arg Ser Leu
325 330 335
Pro Ser Val Glu Thr Leu Gly Cys Thr Ser Val Ile Cys Ser Asp Lys
340 345 350
Thr Gly Thr Leu Thr Thr Asn Gln Met Ser Val Cys Arg Met Phe Ile
355 360 365
Leu Asp Arg Val Glu Gly Asp Thr Cys Ser Leu Asn Glu Phe Thr Ile
370 375 380
Thr Gly Ser Thr Tyr Ala Pro Ile Gly Glu Val His Lys Asp Asp Lys
385 390 395 400
Pro Val Asn Cys His Gln Tyr Asp Gly Leu Val Glu Leu Ala Thr Ile
405 410 415
Cys Ala Leu Cys Asn Asp Ser Ala Leu Asp Tyr Asn Glu Ala Lys Gly
420 425 430
Val Tyr Glu Lys Val Gly Glu Ala Thr Glu Thr Ala Leu Thr Cys Leu
435 440 445
Val Glu Lys Met Asn Val Phe Asp Thr Glu Leu Lys Gly Leu Ser Lys
450 455 460
Ile Glu Arg Ala Asn Ala Cys Asn Ser Val Ile Lys Gln Leu Met Lys
465 470 475 480
Lys Glu Phe Thr Leu Glu Phe Ser Arg Asp Arg Lys Ser Met Ser Val

1241.22

485	490	495
Tyr Cys Thr Pro Asn Lys Pro Ser Arg Thr Ser Met Ser Lys Met Phe		
500	505	510
Val Lys Gly Ala Pro Glu Gly Val Ile Asp Arg Cys Thr His Ile Arg		
515	520	525
Val Gly Ser Thr Lys Val Pro Met Thr Ser Gly Val Lys Gln Lys Ile		
530	535	540
Met Ser Val Ile Arg Glu Trp Gly Ser Gly Ser Asp Thr Leu Arg Cys		
545	550	555
Leu Ala Leu Ala Thr His Asp Asn Pro Leu Arg Arg Glu Glu Met His		
565	570	575
Leu Glu Asp Ser Ala Asn Phe Ile Lys Tyr Glu Thr Asn Leu Thr Phe		
580	585	590
Val Gly Cys Val Gly Met Leu Asp Pro Pro Arg Ile Glu Val Ala Ser		
595	600	605
Ser Val Lys Leu Cys Arg Gln Ala Gly Ile Arg Val Ile Met Ile Thr		
610	615	620
Gly Asp Asn Lys Gly Thr Ala Val Ala Ile Cys Arg Arg Ile Gly Ile		
625	630	635
Phe Gly Gln Asp Glu Asp Val Thr Ser Lys Ala Phe Thr Gly Arg Glu		
645	650	655
Phe Asp Glu Leu Asn Pro Ser Ala Gln Arg Asp Ala Cys Leu Asn Ala		
660	665	670
Arg Cys Phe Ala Arg Val Glu Pro Ser His Lys Ser Lys Ile Val Glu		
675	680	685
Phe Leu Gln Ser Phe Asp Glu Ile Thr Ala Met Thr Gly Asp Gly Val		
690	695	700
Asn Asp Ala Pro Ala Leu Lys Lys Ala Glu Ile Gly Ile Ala Met Gly		
705	710	715
Ser Gly Thr Ala Val Ala Lys Thr Ala Ser Glu Met Val Leu Ala Asp		
725	730	735
Asp Asn Phe Ser Thr Ile Val Ala Ala Val Glu Glu Gly Arg Ala Ile		

1241.22

740	745	750
Tyr Asn Asn Met Lys Gln Phe Ile Arg Tyr Leu Ile Ser Ser Asn Val		
755	760	765
Gly Glu Val Val Cys Ile Phe Leu Thr Ala Ala Leu Gly Phe Pro Glu		
770	775	780
Ala Leu Ile Pro Val Gln Leu Leu Trp Val Asn Leu Val Thr Asp Gly		
785	790	795
800		
Leu Pro Ala Thr Ala Leu Gly Phe Asn Pro Pro Asp Leu Asp Ile Met		
805	810	815
Asn Lys Pro Pro Arg Asn Pro Lys Glu Pro Leu Ile Ser Gly Trp Leu		
820	825	830
Phe Phe Arg Tyr Leu Ala Ile Gly Cys Tyr Val Gly Ala Ala Thr Val		
835	840	845
Gly Ala Ala Ala Trp Trp Phe Ile Ala Ala Asp Gly Gly Pro Arg Val		
850	855	860
Ser Phe Tyr Gln Leu Ser His Phe Leu Gln Cys Lys Glu Asp Asn Pro		
865	870	875
880		
Asp Phe Glu Gly Val Asp Cys Ala Ile Phe Glu Ser Pro Tyr Pro Met		
885	890	895
Thr Met Ala Leu Ser Val Leu Val Thr Ile Glu Met Cys Asn Ala Leu		
900	905	910
Asn Ser Leu Ser Glu Asn Gln Ser Leu Leu Arg Met Pro Pro Trp Glu		
915	920	925
Asn Ile Trp Leu Val Gly Ser Ile Cys Leu Ser Met Ser Leu His Phe		
930	935	940
Leu Ile Leu Tyr Val Glu Pro Leu Pro Leu Ile Phe Gln Ile Thr Pro		
945	950	955
960		
Leu Asn Val Thr Gln Trp Leu Met Val Leu Lys Ile Ser Leu Pro Val		
965	970	975
Ile Leu Met Asp Glu Thr Leu Lys Phe Val Ala Arg Asn Tyr Leu Glu		
980	985	990

Pro Ala Ile Leu Glu

995

<210> 29

<211> 1103

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (133)..(834)

<400> 29

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 ctaggggtca gacaccacca gccaatgagg gagggcacgt ggagccgcgt ctgggctcgc 120
 ggctcctgac ca atg ggg aag tgg cat gtg gga ggg cgc cgg ggt tcc ccc 171

Met Gly Lys Trp His Val Gly Gly Arg Arg Gly Ser Pro

1

5

10

cgc caa tgg gga gct acg gcg cgc ggc cgg gac ttg gag gcg gtg cgg 219
 Arg Gln Trp Gly Ala Thr Ala Arg Gly Arg Asp Leu Glu Ala Val Arg

15

20

25

cgc ggc ggg tgc ggt tca gtc ggt cgg cgg cgg cag cgg agg agg agg 267
 Arg Gly Gly Cys Gly Ser Val Gly Arg Arg Arg Gln Arg Arg Arg Arg

30

35

40

45

agg agg agg agg atg agg agg atg agg agg atg tgg gcc acg cag ggg 315
 Arg Arg Arg Arg Met Arg Arg Met Arg Arg Met Trp Ala Thr Gln Gly

50

55

60

ctg gcg gtg cgc gtg gct ctg agc gtg ctg ccg ggc agc cgg gcg ctg 363
 Leu Ala Val Arg Val Ala Leu Ser Val Leu Pro Gly Ser Arg Ala Leu

65

70

75

cgg ccg ggc gac tgc gaa gtt tgt att tct tat ctg gga aga ttt tac 411
 Arg Pro Gly Asp Cys Glu Val Cys Ile Ser Tyr Leu Gly Arg Phe Tyr

80

85

90

cag gac ctc aaa gac aga gat gtc aca ttc tca cca gcc act att gaa 459

1241.22

Gln Asp Leu Lys Asp Arg Asp Val Thr Phe Ser Pro Ala Thr Ile Glu
95 100 105

aac gaa ctt ata aag ttc tgc cgg gaa gca aga ggc aaa gag aat cgg 507
Asn Glu Leu Ile Lys Phe Cys Arg Glu Ala Arg Gly Lys Glu Asn Arg
110 115 120 125

ttg tgc tac tat atc ggg gcc aca gat gat gca gcc acc aaa atc atc 555
Leu Cys Tyr Tyr Ile Gly Ala Thr Asp Asp Ala Ala Thr Lys Ile Ile
130 135 140

aat gag gta tca aag cct ctg gcc cac cac atc cct gtg gag aag atc 603
Asn Glu Val Ser Lys Pro Leu Ala His His Ile Pro Val Glu Lys Ile
145 150 155

tgt gag aag ctt aag aag aag gac agc cag ata tgt gag ctt aag tat 651
Cys Glu Lys Leu Lys Lys Lys Asp Ser Gln Ile Cys Glu Leu Lys Tyr
160 165 170

gac aag cag atc gac ctg agc aca gtg gac ctg aag aag ctc cga gtt 699
Asp Lys Gln Ile Asp Leu Ser Thr Val Asp Leu Lys Lys Leu Arg Val
175 180 185

aaa gag ctg aag aag att ctg gat gac tgg ggg gag aca tgc aaa ggc 747
Lys Glu Leu Lys Lys Ile Leu Asp Asp Trp Gly Glu Thr Cys Lys Gly
190 195 200 205

tgt gca gaa aag tct gac tac atc cgg aag ata aat gaa ctg atg cct 795
Cys Ala Glu Lys Ser Asp Tyr Ile Arg Lys Ile Asn Glu Leu Met Pro
210 215 220

aaa tat gcc ccc aag gca gcc agt gca ccg acc gat ttg tagtctgctc 844
Lys Tyr Ala Pro Lys Ala Ala Ser Ala Pro Thr Asp Leu
225 230

aatctctgtt gcacctgagg gggaaaaaac agttcaactg cttactccca aaacagcctt 904
tttgtaattt attttttaag tgggctcctg acaatactgt atcagatgtg aagcctggag 964
ctttcctgat gatgctggcc ctacagtacc cccatgaggg gattcccttc cttctgttgc 1024
tggtgtactc taggacttca aagtgtgtct gggatttttt tattaaagaa aaaaaatttc 1084
tagctgtcaa aaaaaaaaaa 1103

1241.22

<210> 30

<211> 234

<212> PRT

<213> Homo sapiens

<400> 30

Met Gly Lys Trp His Val Gly Gly Arg Arg Gly Ser Pro Arg Gln Trp

1 5 10 15

Gly Ala Thr Ala Arg Gly Arg Asp Leu Glu Ala Val Arg Arg Gly Gly

20 25 30

Cys Gly Ser Val Gly Arg Arg Arg Gln Arg Arg Arg Arg Arg Arg

35 40 45

Arg Met Arg Arg Met Arg Arg Met Trp Ala Thr Gln Gly Leu Ala Val

50 55 60

Arg Val Ala Leu Ser Val Leu Pro Gly Ser Arg Ala Leu Arg Pro Gly

65 70 75 80

Asp Cys Glu Val Cys Ile Ser Tyr Leu Gly Arg Phe Tyr Gln Asp Leu

85 90 95

Lys Asp Arg Asp Val Thr Phe Ser Pro Ala Thr Ile Glu Asn Glu Leu

100 105 110

Ile Lys Phe Cys Arg Glu Ala Arg Gly Lys Glu Asn Arg Leu Cys Tyr

115 120 125

Tyr Ile Gly Ala Thr Asp Asp Ala Ala Thr Lys Ile Ile Asn Glu Val

130 135 140

Ser Lys Pro Leu Ala His His Ile Pro Val Glu Lys Ile Cys Glu Lys

145 150 155 160

Leu Lys Lys Lys Asp Ser Gln Ile Cys Glu Leu Lys Tyr Asp Lys Gln

165 170 175

Ile Asp Leu Ser Thr Val Asp Leu Lys Lys Leu Arg Val Lys Glu Leu

180 185 190

Lys Lys Ile Leu Asp Asp Trp Gly Glu Thr Cys Lys Gly Cys Ala Glu

195 200 205

Lys Ser Asp Tyr Ile Arg Lys Ile Asn Glu Leu Met Pro Lys Tyr Ala

1241.22

210 215 220

Pro Lys Ala Ala Ser Ala Pro Thr Asp Leu

225 230

<210> 31

<211> 1860

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (94)..(1266)

<400> 31

cgtgaacggt cgttgcagag attgcgggcg gctgagacgc cgcctgcctg gcacctagga 60

gcgcagcgga gccccgacac cgccgccgcc gcc atg gag tcc gag acc gaa ccc 114

Met Glu Ser Glu Thr Glu Pro

1

5

gag ccc gtc acg ctc ctg gtg aag agc ccc aac cag cgc cac cgc gac 162

Glu Pro Val Thr Leu Leu Val Lys Ser Pro Asn Gln Arg His Arg Asp

10

15

20

ttg gag ctg agt ggc gac cgc ggc tgg agt gtg ggc cac ctc aag gcc 210

Leu Glu Leu Ser Gly Asp Arg Gly Trp Ser Val Gly His Leu Lys Ala

25

30

35

cac ctg agc cgc gtc tac ccc gag cgt ccg cgt cca gag gac cag agg 258

His Leu Ser Arg Val Tyr Pro Glu Arg Pro Arg Pro Glu Asp Gln Arg

40

45

50

55

tta att tat tct ggg aag ctg ttg ttg gat cac caa tgt ctc agg gac 306

Leu Ile Tyr Ser Gly Lys Leu Leu Leu Asp His Gln Cys Leu Arg Asp

60

65

70

ttg ctt cca aag cag gaa aaa cgg cat gtt ttg cat ctg gtg tgc aat 354

Leu Leu Pro Lys Gln Glu Lys Arg His Val Leu His Leu Val Cys Asn

75

80

85

gtg aag agt cct tca aaa atg cca gaa atc aac gcc aag gtg gct gaa 402

Val	Lys	Ser	Pro	Ser	Lys	Met	Pro	Glu	Ile	Asn	Ala	Lys	Val	Ala	Glu	
		90					95					100				
tcc	aca	gag	gag	cct	gct	ggt	tct	aat	cgg	gga	cag	tat	cct	gag	gat	450
Ser	Thr	Glu	Glu	Pro	Ala	Gly	Ser	Asn	Arg	Gly	Gln	Tyr	Pro	Glu	Asp	
		105					110					115				
tcc	tca	agt	gat	ggt	tta	agg	caa	agg	gaa	gtt	ctt	cgg	aac	ctt	tct	498
Ser	Ser	Ser	Asp	Gly	Leu	Arg	Gln	Arg	Glu	Val	Leu	Arg	Asn	Leu	Ser	
120					125					130					135	
tcc	cct	gga	tgg	gaa	aac	atc	tca	agg	cct	gaa	gct	gcc	cag	cag	gca	546
Ser	Pro	Gly	Trp	Glu	Asn	Ile	Ser	Arg	Pro	Glu	Ala	Ala	Gln	Gln	Ala	
				140					145				150			
ttc	caa	ggc	ctg	ggt	cct	ggt	ttc	tcc	ggt	tac	aca	ccc	tat	ggg	tgg	594
Phe	Gln	Gly	Leu	Gly	Pro	Gly	Phe	Ser	Gly	Tyr	Thr	Pro	Tyr	Gly	Trp	
			155					160				165				
ctt	cag	ctt	tcc	tgg	ttc	cag	cag	ata	tat	gca	cga	cag	tac	tac	atg	642
Leu	Gln	Leu	Ser	Trp	Phe	Gln	Gln	Ile	Tyr	Ala	Arg	Gln	Tyr	Tyr	Met	
		170					175				180					
caa	tat	tta	gca	gcc	act	gct	gca	tca	ggg	gct	ttt	gtt	cca	cca	cca	690
Gln	Tyr	Leu	Ala	Ala	Thr	Ala	Ala	Ser	Gly	Ala	Phe	Val	Pro	Pro	Pro	
	185					190				195						
agt	gca	caa	gag	ata	cct	gtg	gtc	tct	gca	cct	gct	cca	gcc	cct	att	738
Ser	Ala	Gln	Glu	Ile	Pro	Val	Val	Ser	Ala	Pro	Ala	Pro	Ala	Pro	Ile	
200				205					210					215		
cac	aac	cag	ttt	cca	gct	gaa	aac	cag	cct	gcc	aat	cag	aat	gct	gct	786
His	Asn	Gln	Phe	Pro	Ala	Glu	Asn	Gln	Pro	Ala	Asn	Gln	Asn	Ala	Ala	
			220					225				230				
cct	caa	gtg	gtt	gtt	aat	cct	gga	gcc	aat	caa	aat	ttg	cgg	atg	aat	834
Pro	Gln	Val	Val	Val	Asn	Pro	Gly	Ala	Asn	Gln	Asn	Leu	Arg	Met	Asn	
		235					240				245					
gca	caa	ggt	ggc	cct	att	gtg	gaa	gaa	gat	gat	gaa	ata	aat	cga	gat	882
Ala	Gln	Gly	Gly	Pro	Ile	Val	Glu	Glu	Asp	Asp	Glu	Ile	Asn	Arg	Asp	

1241.22

250	255	260	
tgg ttg gat tgg acc tat tca gca gct aca ttt tct gtt ttt ctc agt			930
Trp Leu Asp Trp Thr Tyr Ser Ala Ala Thr Phe Ser Val Phe Leu Ser			
265	270	275	
atc ctc tac ttc tac tcc tcc ctg agc aga ttc ctc atg gtc atg ggg			978
Ile Leu Tyr Phe Tyr Ser Ser Leu Ser Arg Phe Leu Met Val Met Gly			
280	285	290	295
gcc acc gtt gtt atg tac ctg cat cac gtt ggg tgg ttt cca ttt aga			1026
Ala Thr Val Val Met Tyr Leu His His Val Gly Trp Phe Pro Phe Arg			
300	305	310	
ccg agg ccg gtt cag aac ttc cca aat gat ggt cct cct cct gac gtt			1074
Pro Arg Pro Val Gln Asn Phe Pro Asn Asp Gly Pro Pro Pro Asp Val			
315	320	325	
gta aat cag gac ccc aac aat aac tta cag gaa ggc act gat cct gaa			1122
Val Asn Gln Asp Pro Asn Asn Asn Leu Gln Glu Gly Thr Asp Pro Glu			
330	335	340	
act gaa gac ccc aac cac ctc cct cca gac agg gat gta cta gat ggc			1170
Thr Glu Asp Pro Asn His Leu Pro Pro Asp Arg Asp Val Leu Asp Gly			
345	350	355	
gag cag acc agc ccc tcc ttt atg agc aca gca tgg ctt gtc ttc aag			1218
Glu Gln Thr Ser Pro Ser Phe Met Ser Thr Ala Trp Leu Val Phe Lys			
360	365	370	375
act ttc ttt gcc tct ctt ctt cca gaa ggc ccc cca gcc atc gca aac			1266
Thr Phe Phe Ala Ser Leu Leu Pro Glu Gly Pro Pro Ala Ile Ala Asn			
380	385	390	
tgatggtggt tgtgctgtag ctgttgagg ctttgacagg aatggactgg atcacctgac			1326
tccagctaga ttgcctctcc tggacatggc aatgatgagt ttttaaaaaa cagtgtggat			1386
gatgatatgc ttttgtgagc aagcaaaagc agaaacgtga agccgtgata caaattggtg			1446
aacaaaaaat gcccaaggct tctcatgtgt ttattctgaa gagctttaat atatactcta			1506
tgtagtttaa taagcactgt acgtagaagg ccttaggtgt tgcattgtcta tgcttgagga			1566
acttttccaa atgtgtgtgt ctgcatgtgt gtttgtacat agaagtcata gatgcagaag			1626
tggttctgct ggtaagattt gattcctggt ggaatgttta aattacacta agtgtactac			1686

1241.22

tttatataat caatgaaatt gctagacatg ttttagcagg acttttctag gaaagactta 1746
tgtataattg ctttttaaaa tgcagtgcctt tacttttaac taaggggaac tttgcggagg 1806
tgaaaacctt tgctggggtt tctgttcaat aaagttttac tatgaatgac cctg 1860

<210> 32

<211> 391

<212> PRT

<213> Homo sapiens

<400> 32

Met Glu Ser Glu Thr Glu Pro Glu Pro Val Thr Leu Leu Val Lys Ser
1 5 10 15
Pro Asn Gln Arg His Arg Asp Leu Glu Leu Ser Gly Asp Arg Gly Trp
20 25 30
Ser Val Gly His Leu Lys Ala His Leu Ser Arg Val Tyr Pro Glu Arg
35 40 45
Pro Arg Pro Glu Asp Gln Arg Leu Ile Tyr Ser Gly Lys Leu Leu Leu
50 55 60
Asp His Gln Cys Leu Arg Asp Leu Leu Pro Lys Gln Glu Lys Arg His
65 70 75 80
Val Leu His Leu Val Cys Asn Val Lys Ser Pro Ser Lys Met Pro Glu
85 90 95
Ile Asn Ala Lys Val Ala Glu Ser Thr Glu Glu Pro Ala Gly Ser Asn
100 105 110
Arg Gly Gln Tyr Pro Glu Asp Ser Ser Ser Asp Gly Leu Arg Gln Arg
115 120 125
Glu Val Leu Arg Asn Leu Ser Ser Pro Gly Trp Glu Asn Ile Ser Arg
130 135 140
Pro Glu Ala Ala Gln Gln Ala Phe Gln Gly Leu Gly Pro Gly Phe Ser
145 150 155 160
Gly Tyr Thr Pro Tyr Gly Trp Leu Gln Leu Ser Trp Phe Gln Gln Ile
165 170 175
Tyr Ala Arg Gln Tyr Tyr Met Gln Tyr Leu Ala Ala Thr Ala Ala Ser

1241.22

180	185	190
Gly Ala Phe Val Pro Pro Pro Ser Ala Gln Glu Ile Pro Val Val Ser		
195	200	205
Ala Pro Ala Pro Ala Pro Ile His Asn Gln Phe Pro Ala Glu Asn Gln		
210	215	220
Pro Ala Asn Gln Asn Ala Ala Pro Gln Val Val Val Asn Pro Gly Ala		
225	230	235
Asn Gln Asn Leu Arg Met Asn Ala Gln Gly Gly Pro Ile Val Glu Glu		
245	250	255
Asp Asp Glu Ile Asn Arg Asp Trp Leu Asp Trp Thr Tyr Ser Ala Ala		
260	265	270
Thr Phe Ser Val Phe Leu Ser Ile Leu Tyr Phe Tyr Ser Ser Leu Ser		
275	280	285
Arg Phe Leu Met Val Met Gly Ala Thr Val Val Met Tyr Leu His His		
290	295	300
Val Gly Trp Phe Pro Phe Arg Pro Arg Pro Val Gln Asn Phe Pro Asn		
305	310	315
Asp Gly Pro Pro Pro Asp Val Val Asn Gln Asp Pro Asn Asn Asn Leu		
325	330	335
Gln Glu Gly Thr Asp Pro Glu Thr Glu Asp Pro Asn His Leu Pro Pro		
340	345	350
Asp Arg Asp Val Leu Asp Gly Glu Gln Thr Ser Pro Ser Phe Met Ser		
355	360	365
Thr Ala Trp Leu Val Phe Lys Thr Phe Phe Ala Ser Leu Leu Pro Glu		
370	375	380
Gly Pro Pro Ala Ile Ala Asn		
385	390	

<210> 33

<211> 4067

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (812)..(1138)

<400> 33

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 cgccacccta ggaggcgcgg tgccaccac tactctgtcc tctgcctgtg ctccgtgccc 180
 gaccctatcc cggcggagtc tccccatcct cttttgcttt ccgactgccc aaggcacttt 240
 caatctcaat ctcttctctc tctctctctc tctctctgtc tctctctctc tctctctctc 300
 tctctctctc gcagggtggg gggaagagga ggaggaattc tttccccgcc taacatttca 360
 agggacacaa ttcactccaa gtctcttccc tttccaagcc gcttccgaag tgctcccggg 420
 gcccgcaact cctgatccca acccgcgaga ggagcctctg cgacctcaaa gcctctcttc 480
 cttctccctc gcttccctcc tcctcttgct acctccacct ccaccgccac ctccacctcc 540
 ggcaccacc caccgccgcc gccgccaccg gcagcgcctc ctctctctct cctctctctc 600
 ccctcttctc tttttggcag ccgctggacg tccggtgttg atggtggcag cggcggcagc 660
 ctaagcaaca gcagccctcg cagcccgcc gctcgcgctc gccccgccgg cgtccccagc 720
 cctatcacct catctcccga aaggtgctgg gcagctccgg ggcggtcgag gcgaagcggc 780
 tgcagcggcg gtagcggcgg cgggaggcag g atg agc gca cgc ggt gag ggc 832

Met Ser Ala Arg Gly Glu Gly

1

5

gcg ggg cag ccg tcc act tca gcc cag gga caa cct gcc gcc cca gcg 880
 Ala Gly Gln Pro Ser Thr Ser Ala Gln Gly Gln Pro Ala Ala Pro Ala

10

15

20

cct cag aag aga gga cgc ggc cgc ccc agg aag cag cag caa gaa cca 928
 Pro Gln Lys Arg Gly Arg Gly Arg Pro Arg Lys Gln Gln Gln Glu Pro

25

30

35

acc ggt gag ccc tct cct aag aga ccc agg gga aga ccc aaa ggc agc 976
 Thr Gly Glu Pro Ser Pro Lys Arg Pro Arg Gly Arg Pro Lys Gly Ser

40

45

50

55

aaa aac aag agt ccc tct aaa gca gct caa aag aaa gca gaa gcc act 1024
 Lys Asn Lys Ser Pro Ser Lys Ala Ala Gln Lys Lys Ala Glu Ala Thr

1241.22

60	65	70	
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Glu Ser Ala Glu Glu Asp			
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gcagcagttg gatcttttga agggagaaga cactgcagtg accacttatt ctgtattgcc 1228			
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<211> 109

<212> PRT

<213> Homo sapiens

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<400> 34

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Arg Lys Gln Gln Gln Glu Pro Thr Gly Glu Pro Ser Pro Lys Arg Pro
35 40 45
Arg Gly Arg Pro Lys Gly Ser Lys Asn Lys Ser Pro Ser Lys Ala Ala
50 55 60
Gln Lys Lys Ala Glu Ala Thr Gly Glu Lys Arg Pro Arg Gly Arg Pro
65 70 75 80
Arg Lys Trp Pro Gln Gln Val Val Gln Lys Lys Pro Ala Gln Glu Glu
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Thr Glu Glu Thr Ser Ser Gln Glu Ser Ala Glu Glu Asp
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<211> 4228

<212> DNA

<213> Homo sapiens

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<222> (148)..(1032)

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cccagctgcc caggaagagc cccagcc atg gaa cac cag ctc ctg tgc tgc gaa 174

Met Glu His Gln Leu Leu Cys Cys Glu

1 5

gtg gaa acc atc cgc cgc gcg tac ccc gat gcc aac ctc ctc aac gac 222
Val Glu Thr Ile Arg Arg Ala Tyr Pro Asp Ala Asn Leu Leu Asn Asp
10 15 20 25

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cgg gtg ctg cgg gcc atg ctg aag gcg gag gag acc tgc gcg ccc tcg	270
Arg Val Leu Arg Ala Met Leu Lys Ala Glu Glu Thr Cys Ala Pro Ser	
30 35 40	
gtg tcc tac ttc aaa tgt gtg cag aag gag gtc ctg ccg tcc atg cgg	318
Val Ser Tyr Phe Lys Cys Val Gln Lys Glu Val Leu Pro Ser Met Arg	
45 50 55	
aag atc gtc gcc acc tgg atg ctg gag gtc tgc gag gaa cag aag tgc	366
Lys Ile Val Ala Thr Trp Met Leu Glu Val Cys Glu Glu Gln Lys Cys	
60 65 70	
gag gag gag gtc ttc ccg ctg gcc atg aac tac ctg gac cgc ttc ctg	414
Glu Glu Glu Val Phe Pro Leu Ala Met Asn Tyr Leu Asp Arg Phe Leu	
75 80 85	
tcg ctg gag ccc gtg aaa aag agc cgc ctg cag ctg ctg ggg gcc act	462
Ser Leu Glu Pro Val Lys Lys Ser Arg Leu Gln Leu Leu Gly Ala Thr	
90 95 100 105	
tgc atg ttc gtg gcc tct aag atg aag gag acc atc ccc ctg acg gcc	510
Cys Met Phe Val Ala Ser Lys Met Lys Glu Thr Ile Pro Leu Thr Ala	
110 115 120	
gag aag ctg tgc atc tac acc gac aac tcc atc cgg ccc gag gag ctg	558
Glu Lys Leu Cys Ile Tyr Thr Asp Asn Ser Ile Arg Pro Glu Glu Leu	
125 130 135	
ctg caa atg gag ctg ctc ctg gtg aac aag ctc aag tgg aac ctg gcc	606
Leu Gln Met Glu Leu Leu Leu Val Asn Lys Leu Lys Trp Asn Leu Ala	
140 145 150	
gca atg acc ccg cac gat ttc att gaa cac ttc ctc tcc aaa atg cca	654
Ala Met Thr Pro His Asp Phe Ile Glu His Phe Leu Ser Lys Met Pro	
155 160 165	
gag gcg gag gag aac aaa cag atc atc cgc aaa cac gcg cag acc ttc	702
Glu Ala Glu Glu Asn Lys Gln Ile Ile Arg Lys His Ala Gln Thr Phe	
170 175 180 185	
gtt gcc ctc tgt gcc aca gat gtg aag ttc att tcc aat ccg ccc tcc	750

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 gtttatgaga tgctggTTTT ctacccaacg gccctgcagc cagctcacgt ccagggttcaa 1992
 cccacagcta cttggTTTTgt gttcttcttc atattctaaa accattccat ttccaagcac 2052
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cttctggaat ttgttcaagt tttgggtatg tttaatctgt tatgtactag tgttctgttt 3672
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<211> 295

<212> PRT

<213> Homo sapiens

<400> 36

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 20 25 30
 Lys Ala Glu Glu Thr Cys Ala Pro Ser Val Ser Tyr Phe Lys Cys Val
 35 40 45
 Gln Lys Glu Val Leu Pro Ser Met Arg Lys Ile Val Ala Thr Trp Met
 50 55 60
 Leu Glu Val Cys Glu Glu Gln Lys Cys Glu Glu Glu Val Phe Pro Leu
 65 70 75 80
 Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Leu Glu Pro Val Lys Lys
 85 90 95
 Ser Arg Leu Gln Leu Leu Gly Ala Thr Cys Met Phe Val Ala Ser Lys
 100 105 110
 Met Lys Glu Thr Ile Pro Leu Thr Ala Glu Lys Leu Cys Ile Tyr Thr

115 120 1241.22 125
 Asp Asn Ser Ile Arg Pro Glu Glu Leu Leu Gln Met Glu Leu Leu Leu
 130 135 140
 Val Asn Lys Leu Lys Trp Asn Leu Ala Ala Met Thr Pro His Asp Phe
 145 150 155 160
 Ile Glu His Phe Leu Ser Lys Met Pro Glu Ala Glu Glu Asn Lys Gln
 165 170 175
 Ile Ile Arg Lys His Ala Gln Thr Phe Val Ala Leu Cys Ala Thr Asp
 180 185 190
 Val Lys Phe Ile Ser Asn Pro Pro Ser Met Val Ala Ala Gly Ser Val
 195 200 205
 Val Ala Ala Val Gln Gly Leu Asn Leu Arg Ser Pro Asn Asn Phe Leu
 210 215 220
 Ser Tyr Tyr Arg Leu Thr Arg Phe Leu Ser Arg Val Ile Lys Cys Asp
 225 230 235 240
 Pro Asp Cys Leu Arg Ala Cys Gln Glu Gln Ile Glu Ala Leu Leu Glu
 245 250 255
 Ser Ser Leu Arg Gln Ala Gln Gln Asn Met Asp Pro Lys Ala Ala Glu
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 Glu Glu Glu Glu Glu Glu Glu Glu Val Asp Leu Ala Cys Thr Pro Thr
 275 280 285
 Asp Val Arg Asp Val Asp Ile
 290 295

<210> 37

<211> 5007

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (436)..(3402)

<400> 37

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 cctcggccccg ggatac atg aaa ggc ctc ggt gac agc cgc ccc cgc cac ctc 471

Met Lys Gly Leu Gly Asp Ser Arg Pro Arg His Leu

1 5 10

tcc gac agc cta gac cca ccc cac gag ccc ctg ttt gca ggg acc gac 519
 Ser Asp Ser Leu Asp Pro Pro His Glu Pro Leu Phe Ala Gly Thr Asp

15 20 25

cgc aac ccc tac ctg ctg tcg ccc acg gag gcc ttc gcc cgc gag gcc 567
 Arg Asn Pro Tyr Leu Leu Ser Pro Thr Glu Ala Phe Ala Arg Glu Ala

30 35 40

cgc ttc ccc ggg cag aac acc ctg cca gga gat ggc ctc ttt ccc ctc 615
 Arg Phe Pro Gly Gln Asn Thr Leu Pro Gly Asp Gly Leu Phe Pro Leu

45 50 55 60

aac aac cag ctg ccc ccg ccc agc agc acc ttt ccc cgc atc cac tac 663
 Asn Asn Gln Leu Pro Pro Pro Ser Ser Thr Phe Pro Arg Ile His Tyr

65 70 75

aac tcc cac ttc gag gtg cca gag gag agc ccc ttc ccc agc cat gcc 711
 Asn Ser His Phe Glu Val Pro Glu Glu Ser Pro Phe Pro Ser His Ala

80 85 90

caa gcc acc aag atc aac cgg ctg ccc gcc aac ctc ctg gac cag ttt 759
 Gln Ala Thr Lys Ile Asn Arg Leu Pro Ala Asn Leu Leu Asp Gln Phe

95 100 105

gag aag cag ctg ccc atc cac cgt gat ggc ttc agc acc ctc caa ttt 807
 Glu Lys Gln Leu Pro Ile His Arg Asp Gly Phe Ser Thr Leu Gln Phe

110 115 120

ccc cgt ggc gag gcc aag gcc cgt ggt gag agc cct ggc cgc atc cgc 855

Pro	Arg	Gly	Glu	Ala	Lys	Ala	Arg	Gly	Glu	Ser	Pro	Gly	Arg	Ile	Arg	
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cac	ctg	gtc	cac	tca	gtc	cag	cgg	ctt	ttc	ttc	acc	aag	gca	ccc	tca	903
His	Leu	Val	His	Ser	Val	Gln	Arg	Leu	Phe	Phe	Thr	Lys	Ala	Pro	Ser	
				145					150					155		
ctg	gag	ggc	aca	gcg	ggc	aag	gtc	ggc	aat	ggc	agc	aag	aag	ggc		951
Leu	Glu	Gly	Thr	Ala	Gly	Lys	Val	Gly	Gly	Asn	Gly	Ser	Lys	Lys	Gly	
				160					165					170		
ggc	atg	gag	gac	ggc	aag	ggc	cgg	agg	gcc	aaa	agc	aag	gag	cgg	gcc	999
Gly	Met	Glu	Asp	Gly	Lys	Gly	Arg	Arg	Ala	Lys	Ser	Lys	Glu	Arg	Ala	
				175					180					185		
aag	gct	ggg	gag	ccc	aaa	cgg	cgc	agc	cgc	tcc	aac	atc	tca	ggc	tgg	1047
Lys	Ala	Gly	Glu	Pro	Lys	Arg	Arg	Ser	Arg	Ser	Asn	Ile	Ser	Gly	Trp	
				190										200		
tgg	agc	tcc	gat	gac	aac	ttg	gac	ggc	gag	gcc	ggc	gcc	ttc	cgc	agc	1095
Trp	Ser	Ser	Asp	Asp	Asn	Leu	Asp	Gly	Glu	Ala	Gly	Ala	Phe	Arg	Ser	
205					210				215					220		
agt	ggc	cca	gcc	tct	ggg	ctg	atg	ata	cta	ggc	cgc	cag	gca	gaa	cgc	1143
Ser	Gly	Pro	Ala	Ser	Gly	Leu	Met	Ile	Leu	Gly	Arg	Gln	Ala	Glu	Arg	
					225					230				235		
agc	cag	cca	cgc	tac	ttc	atg	cac	gcc	tac	aac	acc	atc	agt	ggg	cac	1191
Ser	Gln	Pro	Arg	Tyr	Phe	Met	His	Ala	Tyr	Asn	Thr	Ile	Ser	Gly	His	
				240					245					250		
atg	ctc	aaa	acc	acc	aag	aac	aac	act	act	gag	ctg	act	gcc	cca	cca	1239
Met	Leu	Lys	Thr	Thr	Lys	Asn	Asn	Thr	Thr	Glu	Leu	Thr	Ala	Pro	Pro	
				255					260					265		
ccc	ccg	ccc	gca	ccc	cca	gcc	acc	tgc	ccc	agc	ctt	ggg	gtg	ggc	act	1287
Pro	Pro	Pro	Ala	Pro	Pro	Ala	Thr	Cys	Pro	Ser	Leu	Gly	Val	Gly	Thr	
				270					275					280		
gac	acc	aac	tac	gtc	aaa	cgg	ggc	tcc	tgg	tcc	act	ctg	acc	ctc	agc	1335
Asp	Thr	Asn	Tyr	Val	Lys	Arg	Gly	Ser	Trp	Ser	Thr	Leu	Thr	Leu	Ser	

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cac gcc cac gag gtc tgc cag aag acc tca gcc acc ttg gat aag agc				1383
His Ala His Glu Val Cys Gln Lys Thr Ser Ala Thr Leu Asp Lys Ser				
	305	310	315	
ctg ctc aag tcc aaa tcc tgc cac cag ggt cta gcc tac cat tac ctg				1431
Leu Leu Lys Ser Lys Ser Cys His Gln Gly Leu Ala Tyr His Tyr Leu				
	320	325	330	
cag gtg ccc ggc ggc ggc ggc gag tgg agc acc acg ctg ctg tcc cca				1479
Gln Val Pro Gly Gly Gly Gly Glu Trp Ser Thr Thr Leu Leu Ser Pro				
	335	340	345	
cgc gag acg gat gcc gcg gcc gag ggc cct atc ccg tgc cgg cgc atg				1527
Arg Glu Thr Asp Ala Ala Ala Glu Gly Pro Ile Pro Cys Arg Arg Met				
	350	355	360	
cgc agc ggc agc tac atc aag gcc atg ggc gac gag gac agc gac gag				1575
Arg Ser Gly Ser Tyr Ile Lys Ala Met Gly Asp Glu Asp Ser Asp Glu				
365	370	375	380	
tcc ggc ggc agc ccc aag ccc tca ccc aag acc gcg gcg cgg cgc cag				1623
Ser Gly Gly Ser Pro Lys Pro Ser Pro Lys Thr Ala Ala Arg Arg Gln				
	385	390	395	
agc tat ctg agg gcc acg cag cag tcg ctg gga gag cag agc aac ccc				1671
Ser Tyr Leu Arg Ala Thr Gln Gln Ser Leu Gly Glu Gln Ser Asn Pro				
	400	405	410	
cgc agg agt ctg gac cgc ctg gat tca gtg gac atg ctg ctg ccc tcc				1719
Arg Arg Ser Leu Asp Arg Leu Asp Ser Val Asp Met Leu Leu Pro Ser				
	415	420	425	
aag tgt ccg agc tgg gaa gag gac tac acc ccc gtc agc gac agc ctc				1767
Lys Cys Pro Ser Trp Glu Glu Asp Tyr Thr Pro Val Ser Asp Ser Leu				
	430	435	440	
aac gac tcc agc tgc atc agc cag att ttt gga cag gcc tcc ctg atc				1815
Asn Asp Ser Ser Cys Ile Ser Gln Ile Phe Gly Gln Ala Ser Leu Ile				
445	450	455	460	
ccc cag ttg ttt ggc cat gag cag cag gta cgg gag gca gag ctg agt				1863

Pro	Gln	Leu	Phe	Gly	His	Glu	Gln	Gln	Val	Arg	Glu	Ala	Glu	Leu	Ser		
				465			470										
gac	cag	tat	gag	gcg	gcc	tgc	gag	tca	gcc	tgc	agt	gaa	gcg	gag	tcc	1911	
Asp	Gln	Tyr	Glu	Ala	Ala	Cys	Glu	Ser	Ala	Cys	Ser	Glu	Ala	Glu	Ser		
				480			485										
aca	gcg	gca	gag	acg	ctt	gac	ttg	cca	ctg	ccc	agc	tac	ttc	cgc	tcc	1959	
Thr	Ala	Ala	Glu	Thr	Leu	Asp	Leu	Pro	Leu	Pro	Ser	Tyr	Phe	Arg	Ser		
				495			500										
cgc	agc	cac	agc	tac	ctg	cgt	gcc	atc	cag	gca	ggc	tgc	tcg	cag	gag	2007	
Arg	Ser	His	Ser	Tyr	Leu	Arg	Ala	Ile	Gln	Ala	Gly	Cys	Ser	Gln	Glu		
				510			515										
gag	gac	agt	gtc	tcc	ctg	cag	tcc	ctc	tcc	cca	ccg	ccc	agt	acc	ggc	2055	
Glu	Asp	Ser	Val	Ser	Leu	Gln	Ser	Leu	Ser	Pro	Pro	Pro	Ser	Thr	Gly		
525				530				535				540					
agc	ctc	agc	aat	agt	cgc	acg	ctt	ccg	agt	tca	tca	tgc	cta	gtg	gcg	2103	
Ser	Leu	Ser	Asn	Ser	Arg	Thr	Leu	Pro	Ser	Ser	Ser	Cys	Leu	Val	Ala		
				545			550										
tat	aag	aag	acc	ccg	cca	ccg	gtc	cct	cca	cgc	acc	act	tca	aag	ccg	2151	
Tyr	Lys	Lys	Thr	Pro	Pro	Pro	Val	Pro	Pro	Arg	Thr	Thr	Ser	Lys	Pro		
				560			565										
ttc	atc	tca	gtc	aca	gtc	cag	agc	agt	act	gag	tct	gcc	cag	gac	acc	2199	
Phe	Ile	Ser	Val	Thr	Val	Gln	Ser	Ser	Thr	Glu	Ser	Ala	Gln	Asp	Thr		
				575			580										
tac	ctg	gac	agc	cag	gac	cac	aag	agc	gag	gtg	act	agc	cag	tcg	ggc	2247	
Tyr	Leu	Asp	Ser	Gln	Asp	His	Lys	Ser	Glu	Val	Thr	Ser	Gln	Ser	Gly		
				590			595										
ctg	agc	aac	tcg	tcg	gac	agc	ctg	gac	agc	agt	acc	cga	ccg	ccc	agc	2295	
Leu	Ser	Asn	Ser	Ser	Asp	Ser	Leu	Asp	Ser	Ser	Thr	Arg	Pro	Pro	Ser		
605				610				615				620					
gtg	aca	cgg	ggt	gga	gtc	gcc	cca	gcc	cct	gag	gcc	cca	gag	cca	ccc	2343	
Val	Thr	Arg	Gly	Gly	Val	Ala	Pro	Ala	Pro	Glu	Ala	Pro	Glu	Pro	Pro		

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625	630	635	
cca aaa cat gca gct ctg aaa agt gaa caa ggg acg ctg acc agc tct			2391
Pro Lys His Ala Ala Leu Lys Ser Glu Gln Gly Thr Leu Thr Ser Ser			
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gag tcc cac ccc gag gcc gcc ccc aaa agg aaa ctg tca tcg ata gga			2439
Glu Ser His Pro Glu Ala Ala Pro Lys Arg Lys Leu Ser Ser Ile Gly			
655	660	665	
ata caa gag agg act aga agg aac ggt tcc cac ctc tcg gag gac aac			2487
Ile Gln Glu Arg Thr Arg Arg Asn Gly Ser His Leu Ser Glu Asp Asn			
670	675	680	
gga ccc aaa gcg atc gat gtg atg gca ccc tcc tca gaa agc agc gtc			2535
Gly Pro Lys Ala Ile Asp Val Met Ala Pro Ser Ser Glu Ser Ser Val			
685	690	695	700
ccc tct cac agt atg tcc tcc cga cgg gac aca gac tcg gat acc cag			2583
Pro Ser His Ser Met Ser Ser Arg Arg Asp Thr Asp Ser Asp Thr Gln			
705	710	715	
gat gcc aat gac tca agc tgt aag tca tct gag agg agc ctc ccg gac			2631
Asp Ala Asn Asp Ser Ser Cys Lys Ser Ser Glu Arg Ser Leu Pro Asp			
720	725	730	
tgt acc cct cac ccc aac tcc atc agc atc gat gcc ggt ccc cgg cag			2679
Cys Thr Pro His Pro Asn Ser Ile Ser Ile Asp Ala Gly Pro Arg Gln			
735	740	745	
gcc ccc aag att gcc cag atc aag cgc aac ctc tcc tat gga gac aac			2727
Ala Pro Lys Ile Ala Gln Ile Lys Arg Asn Leu Ser Tyr Gly Asp Asn			
750	755	760	
agc gac cct gcc cta gag gcg tcc tcg ctg ccc cca ccc gac ccc tgg			2775
Ser Asp Pro Ala Leu Glu Ala Ser Ser Leu Pro Pro Pro Asp Pro Trp			
765	770	775	780
ctc gag acc tcc tcc agc tcc cca gca gag ccg gca cag cca ggg gcc			2823
Leu Glu Thr Ser Ser Ser Ser Pro Ala Glu Pro Ala Gln Pro Gly Ala			
785	790	795	
tgc cgc cga gac ggc tac tgg ttc cta aag cta ctg cag gca gaa aca			2871

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 Cys Arg Arg Asp Gly Tyr Trp Phe Leu Lys Leu Leu Gln Ala Glu Thr
 800 805 810 2919
 gag cgg ctg gaa ggc tgg tgc tgc cag atg gac aag gag acc aaa gag
 Glu Arg Leu Glu Gly Trp Cys Cys Gln Met Asp Lys Glu Thr Lys Glu
 815 820 825 2967
 aac aac ctc tct gaa gaa gtc tta gga aaa gtc ctc agt gct gtg ggc
 Asn Asn Leu Ser Glu Glu Val Leu Gly Lys Val Leu Ser Ala Val Gly
 830 835 840 3015
 agt gcc cag cta ctg atg tcc cag aaa ttc cag cag ttc cgg ggc ctc
 Ser Ala Gln Leu Leu Met Ser Gln Lys Phe Gln Gln Phe Arg Gly Leu
 845 850 855 3063
 tgt gag caa aac ttg aac cct gat gcc aac cca cgc ccc aca gcc cag
 Cys Glu Gln Asn Leu Asn Pro Asp Ala Asn Pro Arg Pro Thr Ala Gln
 865 870 875 3111
 gac ctg gca ggg ttc tgg gac ctg cta cag ctg tcc atc gag gat atc
 Asp Leu Ala Gly Phe Trp Asp Leu Leu Gln Leu Ser Ile Glu Asp Ile
 880 885 890 3159
 agc atg aag ttc gat gaa ctc tac cac ctc aag gcc aac agc tgg cag
 Ser Met Lys Phe Asp Glu Leu Tyr His Leu Lys Ala Asn Ser Trp Gln
 895 900 905 3207
 ctg gtg gag acc ccc gag aag agg aag gaa gag aag aaa cca ccc cct
 Leu Val Glu Thr Pro Glu Lys Arg Lys Glu Glu Lys Lys Pro Pro Pro
 910 915 920 3255
 ccg gtc cca aag aag cca gcc aaa tcc aag ccg gca gtg agc cgc gac
 Pro Val Pro Lys Lys Pro Ala Lys Ser Lys Pro Ala Val Ser Arg Asp
 925 930 935 3303
 aag gcc tca gac gcc agc gac aag cag cgc cag gag gcc cgc aag aga
 Lys Ala Ser Asp Ala Ser Asp Lys Gln Arg Gln Glu Ala Arg Lys Arg
 945 950 955 3351
 ctc ctg gcg gcc aag cgg gca gct tct gtg cgg cag aac tca gcc acc
 Leu Leu Ala Ala Lys Arg Ala Ala Ser Val Arg Gln Asn Ser Ala Thr

1241.22

960	965	970	
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gag agc gca gac agc atc gag att tat gtc ccg gag gcc cag acc agg 3399
 Glu Ser Ala Asp Ser Ile Glu Ile Tyr Val Pro Glu Ala Gln Thr Arg

975	980	985	
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ctc tgagaccatg caggaggaaa gaaacgattt taaatcatta aaaacacaaa 3452
 Leu

aactaagtgc gaacggaaca gagttttctc aacctttgct atggttattc tgtctagaga 3512
 ccctgagcca actttcaaat tgacgcatac aagggctcac aatttggtt ttttgggtcc 3572
 ctcccagctt taggttatga agattttact cacaaaaaaa atcaacaaaa atcacgaaac 3632
 tagaaaactt tttttttcct cttgctggcc gtgggtggact agatagatgg acgtcggcaa 3692
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1241.22

<210> 38

<211> 989

<212> PRT

<213> Homo sapiens

<400> 38

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Leu Leu Ser Pro Thr Glu Ala Phe Ala Arg Glu Ala Arg Phe Pro Gly
35 40 45
Gln Asn Thr Leu Pro Gly Asp Gly Leu Phe Pro Leu Asn Asn Gln Leu
50 55 60
Pro Pro Pro Ser Ser Thr Phe Pro Arg Ile His Tyr Asn Ser His Phe
65 70 75 80
Glu Val Pro Glu Glu Ser Pro Phe Pro Ser His Ala Gln Ala Thr Lys
85 90 95
Ile Asn Arg Leu Pro Ala Asn Leu Leu Asp Gln Phe Glu Lys Gln Leu
100 105 110
Pro Ile His Arg Asp Gly Phe Ser Thr Leu Gln Phe Pro Arg Gly Glu
115 120 125
Ala Lys Ala Arg Gly Glu Ser Pro Gly Arg Ile Arg His Leu Val His
130 135 140
Ser Val Gln Arg Leu Phe Phe Thr Lys Ala Pro Ser Leu Glu Gly Thr
145 150 155 160
Ala Gly Lys Val Gly Gly Asn Gly Ser Lys Lys Gly Gly Met Glu Asp
165 170 175
Gly Lys Gly Arg Arg Ala Lys Ser Lys Glu Arg Ala Lys Ala Gly Glu
180 185 190
Pro Lys Arg Arg Ser Arg Ser Asn Ile Ser Gly Trp Trp Ser Ser Asp
195 200 205

1241.22

Asp Asn Leu Asp Gly Glu Ala Gly Ala Phe Arg Ser Ser Gly Pro Ala
210 215 220
Ser Gly Leu Met Ile Leu Gly Arg Gln Ala Glu Arg Ser Gln Pro Arg
225 230 235 240
Tyr Phe Met His Ala Tyr Asn Thr Ile Ser Gly His Met Leu Lys Thr
245 250 255
Thr Lys Asn Asn Thr Thr Glu Leu Thr Ala Pro Pro Pro Pro Pro Ala
260 265 270
Pro Pro Ala Thr Cys Pro Ser Leu Gly Val Gly Thr Asp Thr Asn Tyr
275 280 285
Val Lys Arg Gly Ser Trp Ser Thr Leu Thr Leu Ser His Ala His Glu
290 295 300
Val Cys Gln Lys Thr Ser Ala Thr Leu Asp Lys Ser Leu Leu Lys Ser
305 310 315 320
Lys Ser Cys His Gln Gly Leu Ala Tyr His Tyr Leu Gln Val Pro Gly
325 330 335
Gly Gly Gly Glu Trp Ser Thr Thr Leu Leu Ser Pro Arg Glu Thr Asp
340 345 350
Ala Ala Ala Glu Gly Pro Ile Pro Cys Arg Arg Met Arg Ser Gly Ser
355 360 365
Tyr Ile Lys Ala Met Gly Asp Glu Asp Ser Asp Glu Ser Gly Gly Ser
370 375 380
Pro Lys Pro Ser Pro Lys Thr Ala Ala Arg Arg Gln Ser Tyr Leu Arg
385 390 395 400
Ala Thr Gln Gln Ser Leu Gly Glu Gln Ser Asn Pro Arg Arg Ser Leu
405 410 415
Asp Arg Leu Asp Ser Val Asp Met Leu Leu Pro Ser Lys Cys Pro Ser
420 425 430
Trp Glu Glu Asp Tyr Thr Pro Val Ser Asp Ser Leu Asn Asp Ser Ser
435 440 445
Cys Ile Ser Gln Ile Phe Gly Gln Ala Ser Leu Ile Pro Gln Leu Phe

1241.22
460

450 455
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465 470 475 480
Ala Ala Cys Glu Ser Ala Cys Ser Glu Ala Glu Ser Thr Ala Ala Glu
485 490 495
Thr Leu Asp Leu Pro Leu Pro Ser Tyr Phe Arg Ser Arg Ser His Ser
500 505 510
Tyr Leu Arg Ala Ile Gln Ala Gly Cys Ser Gln Glu Glu Asp Ser Val
515 520 525
Ser Leu Gln Ser Leu Ser Pro Pro Pro Ser Thr Gly Ser Leu Ser Asn
530 535 540
Ser Arg Thr Leu Pro Ser Ser Ser Cys Leu Val Ala Tyr Lys Lys Thr
545 550 555 560
Pro Pro Pro Val Pro Pro Arg Thr Thr Ser Lys Pro Phe Ile Ser Val
565 570 575
Thr Val Gln Ser Ser Thr Glu Ser Ala Gln Asp Thr Tyr Leu Asp Ser
580 585 590
Gln Asp His Lys Ser Glu Val Thr Ser Gln Ser Gly Leu Ser Asn Ser
595 600 605
Ser Asp Ser Leu Asp Ser Ser Thr Arg Pro Pro Ser Val Thr Arg Gly
610 615 620
Gly Val Ala Pro Ala Pro Glu Ala Pro Glu Pro Pro Pro Lys His Ala
625 630 635 640
Ala Leu Lys Ser Glu Gln Gly Thr Leu Thr Ser Ser Glu Ser His Pro
645 650 655
Glu Ala Ala Pro Lys Arg Lys Leu Ser Ser Ile Gly Ile Gln Glu Arg
660 665 670
Thr Arg Arg Asn Gly Ser His Leu Ser Glu Asp Asn Gly Pro Lys Ala
675 680 685
Ile Asp Val Met Ala Pro Ser Ser Glu Ser Ser Val Pro Ser His Ser
690 695 700
Met Ser Ser Arg Arg Asp Thr Asp Ser Asp Thr Gln Asp Ala Asn Asp
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705 710 715 720
Ser Ser Cys Lys Ser Ser Glu Arg Ser Leu Pro Asp Cys Thr Pro His
725 730 735
Pro Asn Ser Ile Ser Ile Asp Ala Gly Pro Arg Gln Ala Pro Lys Ile
740 745 750
Ala Gln Ile Lys Arg Asn Leu Ser Tyr Gly Asp Asn Ser Asp Pro Ala
755 760 765
Leu Glu Ala Ser Ser Leu Pro Pro Pro Asp Pro Trp Leu Glu Thr Ser
770 775 780
Ser Ser Ser Pro Ala Glu Pro Ala Gln Pro Gly Ala Cys Arg Arg Asp
785 790 795 800
Gly Tyr Trp Phe Leu Lys Leu Leu Gln Ala Glu Thr Glu Arg Leu Glu
805 810 815
Gly Trp Cys Cys Gln Met Asp Lys Glu Thr Lys Glu Asn Asn Leu Ser
820 825 830
Glu Glu Val Leu Gly Lys Val Leu Ser Ala Val Gly Ser Ala Gln Leu
835 840 845
Leu Met Ser Gln Lys Phe Gln Gln Phe Arg Gly Leu Cys Glu Gln Asn
850 855 860
Leu Asn Pro Asp Ala Asn Pro Arg Pro Thr Ala Gln Asp Leu Ala Gly
865 870 875 880
Phe Trp Asp Leu Leu Gln Leu Ser Ile Glu Asp Ile Ser Met Lys Phe
885 890 895
Asp Glu Leu Tyr His Leu Lys Ala Asn Ser Trp Gln Leu Val Glu Thr
900 905 910
Pro Glu Lys Arg Lys Glu Glu Lys Lys Pro Pro Pro Val Pro Lys
915 920 925
Lys Pro Ala Lys Ser Lys Pro Ala Val Ser Arg Asp Lys Ala Ser Asp
930 935 940
Ala Ser Asp Lys Gln Arg Gln Glu Ala Arg Lys Arg Leu Leu Ala Ala
945 950 955 960

1241.22

Lys Arg Ala Ala Ser Val Arg Gln Asn Ser Ala Thr Glu Ser Ala Asp
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Ser Ile Glu Ile Tyr Val Pro Glu Ala Gln Thr Arg Leu
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<210> 39

<211> 2522

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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<400> 39

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cgg ggc cag gtg gcc aag ctt gag gca gcc cta ggt gag gcc aag aag	96
Arg Gly Gln Val Ala Lys Leu Glu Ala Ala Leu Gly Glu Ala Lys Lys	
20 25 30	
caa ctt cag gat gag atg ctg cgg cgg gtg gat gct gag aac agg ctg	144
Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp Ala Glu Asn Arg Leu	
35 40 45	
cag acc atg aag gag gaa ctg gac ttc cag aag aac atc tac agt gag	192
Gln Thr Met Lys Glu Glu Leu Asp Phe Gln Lys Asn Ile Tyr Ser Glu	
50 55 60	
gag ctg cgt gag acc aag cgc cgt cat gag acc cga ctg gtg gag att	240
Glu Leu Arg Glu Thr Lys Arg Arg His Glu Thr Arg Leu Val Glu Ile	
65 70 75 80	
gac aat ggg aag cag cgt gag ttt gag agc cgg ctg gcg gat gcg ctg	288
Asp Asn Gly Lys Gln Arg Glu Phe Glu Ser Arg Leu Ala Asp Ala Leu	
85 90 95	
cag gaa ctg cgg gcc cag cat gag gac cag gtg gag cag tat aag aag	336

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Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val Glu Gln Tyr Lys Lys	
100 105 110	
gag ctg gag aag act tat tct gcc aag ctg gac aat gcc agg cag tct	384
Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp Asn Ala Arg Gln Ser	
115 120 125	
gct gag agg aac agc aac ctg gtg ggg gct gcc cac gag gag ctg cag	432
Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala His Glu Glu Leu Gln	
130 135 140	
cag tcg cgc atc cgc atc gac agc ctc tct gcc cag ctc agc cag ctc	480
Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala Gln Leu Ser Gln Leu	
145 150 155 160	
cag aag cag ctg gca gcc aag gag gcg aag ctt cga gac ctg gag gac	528
Gln Lys Gln Leu Ala Ala Lys Glu Ala Lys Leu Arg Asp Leu Glu Asp	
165 170 175	
tca ctg gcc cgt gag cgg gac acc agc cgg cgg ctg ctg gcg gaa aag	576
Ser Leu Ala Arg Glu Arg Asp Thr Ser Arg Arg Leu Leu Ala Glu Lys	
180 185 190	
gag cgg gag atg gcc gag atg cgg gca agg atg cag cag cag ctg gac	624
Glu Arg Glu Met Ala Glu Met Arg Ala Arg Met Gln Gln Gln Leu Asp	
195 200 205	
gag tac cag gag ctt ctg gac atc aag ctg gcc ctg gac atg gag atc	672
Glu Tyr Gln Glu Leu Leu Asp Ile Lys Leu Ala Leu Asp Met Glu Ile	
210 215 220	
cac gcc tac cgc aag ctc ttg gag ggc gag gag gag agg cta cgc ctg	720
His Ala Tyr Arg Lys Leu Leu Glu Gly Glu Glu Glu Arg Leu Arg Leu	
225 230 235 240	
tcc ccc agc cct acc tcg cag cgc agc cgt ggc cgt gct tcc tct cac	768
Ser Pro Ser Pro Thr Ser Gln Arg Ser Arg Gly Arg Ala Ser Ser His	
245 250 255	
tca tcc cag aca cag ggt ggg ggc agc gtc acc aaa aag cgc aaa ctg	816
Ser Ser Gln Thr Gln Gly Gly Gly Ser Val Thr Lys Lys Arg Lys Leu	
260 265 270	

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gag tcc act gag agc cgc agc agc ttc tca cag cac gca cgc act agc	864
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275 280 285	
ggg cgc gtg gcc gtg gag gag gtg gat gag gag ggc aag ttt gtc cgg	912
Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu Gly Lys Phe Val Arg	
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ctg cgc aac aag tcc aat gag gac cag tcc atg ggc aat tgg cag atc	960
Leu Arg Asn Lys Ser Asn Glu Asp Gln Ser Met Gly Asn Trp Gln Ile	
305 310 315 320	
aag cgc cag aat gga gat gat ccc ttg ctg act tac cgg ttc cca cca	1008
Lys Arg Gln Asn Gly Asp Asp Pro Leu Leu Thr Tyr Arg Phe Pro Pro	
325 330 335	
aag ttc acc ctg aag gct ggg cag gtg gtg acg atc tgg gct gca gga	1056
Lys Phe Thr Leu Lys Ala Gly Gln Val Val Thr Ile Trp Ala Ala Gly	
340 345 350	
gct ggg gcc acc cac agc ccc cct acc gac ctg gtg tgg aag gca cag	1104
Ala Gly Ala Thr His Ser Pro Pro Thr Asp Leu Val Trp Lys Ala Gln	
355 360 365	
aac acc tgg ggc tgc ggg aac agc ctg cgt acg gct ctc atc aac tcc	1152
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Thr Gly Glu Glu Val Ala Met Arg Lys Leu Val Arg Ser Val Thr Val	
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gtt gag gac gac gag gat gag gat gga gat gac ctg ctc cat cac cac	1248
Val Glu Asp Asp Glu Asp Glu Asp Gly Asp Asp Leu Leu His His His	
405 410 415	
cac ggc tcc cac tgc agc agc tcg ggg gac ccc gct gag tac aac ctg	1296
His Gly Ser His Cys Ser Ser Ser Gly Asp Pro Ala Glu Tyr Asn Leu	
420 425 430	
cgc tcg cgc acc gtg ctg tgc ggg acc tgc ggg cag cct gcc gac aag	1344

1241.22

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435 440 445

gca tct gcc agc ggc tca gga gcc cag gtg ggc gga ccc atc tcc tct 1392
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450 455 460

ggc tct tct gcc tcc agt gtc acg gtc act cgc agc tac cgc agt gtg 1440
Gly Ser Ser Ala Ser Ser Val Thr Val Thr Arg Ser Tyr Arg Ser Val
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ggg ggc agt ggg ggt ggc agc ttc ggg gac aat ctg gtc acc cgc tcc 1488
Gly Gly Ser Gly Gly Gly Ser Phe Gly Asp Asn Leu Val Thr Arg Ser
485 490 495

tac ctc ctg ggc aac tcc agc ccc cga acc cag agc ccc cag aac tgc 1536
Tyr Leu Leu Gly Asn Ser Ser Pro Arg Thr Gln Ser Pro Gln Asn Cys
500 505 510

agc atc atg taatctggga cctgccaggc aggggtgggg gtggaggctt 1585
Ser Ile Met
515

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1241.22

2522

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<210> 40

<211> 515

<212> PRT

<213> Homo sapiens

<400> 40

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Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp Ala Glu Asn Arg Leu
35 40 45
Gln Thr Met Lys Glu Glu Leu Asp Phe Gln Lys Asn Ile Tyr Ser Glu
50 55 60
Glu Leu Arg Glu Thr Lys Arg Arg His Glu Thr Arg Leu Val Glu Ile
65 70 75 80
Asp Asn Gly Lys Gln Arg Glu Phe Glu Ser Arg Leu Ala Asp Ala Leu
85 90 95
Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val Glu Gln Tyr Lys Lys
100 105 110
Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp Asn Ala Arg Gln Ser
115 120 125
Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala His Glu Glu Leu Gln
130 135 140
Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala Gln Leu Ser Gln Leu
145 150 155 160
Gln Lys Gln Leu Ala Ala Lys Glu Ala Lys Leu Arg Asp Leu Glu Asp
165 170 175
Ser Leu Ala Arg Glu Arg Asp Thr Ser Arg Arg Leu Leu Ala Glu Lys
180 185 190
Glu Arg Glu Met Ala Glu Met Arg Ala Arg Met Gln Gln Gln Leu Asp

1241.22

195 200 205
Glu Tyr Gln Glu Leu Leu Asp Ile Lys Leu Ala Leu Asp Met Glu Ile
210 215 220
His Ala Tyr Arg Lys Leu Leu Glu Gly Glu Glu Glu Arg Leu Arg Leu
225 230 235 240
Ser Pro Ser Pro Thr Ser Gln Arg Ser Arg Gly Arg Ala Ser Ser His
245 250 255
Ser Ser Gln Thr Gln Gly Gly Gly Ser Val Thr Lys Lys Arg Lys Leu
260 265 270
Glu Ser Thr Glu Ser Arg Ser Ser Phe Ser Gln His Ala Arg Thr Ser
275 280 285
Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu Gly Lys Phe Val Arg
290 295 300
Leu Arg Asn Lys Ser Asn Glu Asp Gln Ser Met Gly Asn Trp Gln Ile
305 310 315 320
Lys Arg Gln Asn Gly Asp Asp Pro Leu Leu Thr Tyr Arg Phe Pro Pro
325 330 335
Lys Phe Thr Leu Lys Ala Gly Gln Val Val Thr Ile Trp Ala Ala Gly
340 345 350
Ala Gly Ala Thr His Ser Pro Pro Thr Asp Leu Val Trp Lys Ala Gln
355 360 365
Asn Thr Trp Gly Cys Gly Asn Ser Leu Arg Thr Ala Leu Ile Asn Ser
370 375 380
Thr Gly Glu Glu Val Ala Met Arg Lys Leu Val Arg Ser Val Thr Val
385 390 395 400
Val Glu Asp Asp Glu Asp Glu Asp Gly Asp Asp Leu Leu His His His
405 410 415
His Gly Ser His Cys Ser Ser Ser Gly Asp Pro Ala Glu Tyr Asn Leu
420 425 430
Arg Ser Arg Thr Val Leu Cys Gly Thr Cys Gly Gln Pro Ala Asp Lys
435 440 445

1241.22

Ala Ser Ala Ser Gly Ser Gly Ala Gln Val Gly Gly Pro Ile Ser Ser
 450 455 460

Gly Ser Ser Ala Ser Ser Val Thr Val Thr Arg Ser Tyr Arg Ser Val
 465 470 475 480

Gly Gly Ser Gly Gly Gly Ser Phe Gly Asp Asn Leu Val Thr Arg Ser
 485 490 495

Tyr Leu Leu Gly Asn Ser Ser Pro Arg Thr Gln Ser Pro Gln Asn Cys
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Ser Ile Met
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 cgagcgagag gcgcgga atg gtg gac tac cac gcg gcg aac cag tcg tac 110
 Met Val Asp Tyr His Ala Ala Asn Gln Ser Tyr
 1 5 10
 cag tac ggc ccc agc agc gcg gca atg gct tgg cgg cgg ggg agc atg 158
 Gln Tyr Gly Pro Ser Ser Ala Ala Met Ala Trp Arg Arg Gly Ser Met
 15 20 25
 ggc gac tac atg gcc cag gag gac gac tgg gac cgg gac ctg ctg ctg 206
 Gly Asp Tyr Met Ala Gln Glu Asp Asp Trp Asp Arg Asp Leu Leu Leu
 30 35 40
 gac ccg gcc tgg gag aag cag cag cgc aag acc ttc acg gca tgg agc 254
 Asp Pro Ala Trp Glu Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Ser
 45 50 55

1241.22

aac tcc cac ctg cgg aag gca ggc aca cag atc gag aac att gat gag	302
Asn Ser His Leu Arg Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp Glu	
60 65 70 75	
gac ttc cga gac ggg ctc aag ctc atg ctg ctc ctg gag gtc ata tca	350
Asp Phe Arg Asp Gly Leu Lys Leu Met Leu Leu Leu Glu Val Ile Ser	
80 85 90	
ggg gag cgg tta cct aag ccg gag cgg ggg aag atg aga gtg cac aaa	398
Gly Glu Arg Leu Pro Lys Pro Glu Arg Gly Lys Met Arg Val His Lys	
95 100 105	
atc aac aat gtg aac aaa gcg ctg gac ttt att gcc agc aaa ggg atc	446
Ile Asn Asn Val Asn Lys Ala Leu Asp Phe Ile Ala Ser Lys Gly Ile	
110 115 120	
aag ctg gac ttc cat cgg gca gaa gag att gtg gac ggc aac gca aag	494
Lys Leu Asp Phe His Arg Ala Glu Glu Ile Val Asp Gly Asn Ala Lys	
125 130 135	
atg acc ctg gga atg atc tgg acc atc atc ctt agg ttc gcc atc cag	542
Met Thr Leu Gly Met Ile Trp Thr Ile Ile Leu Arg Phe Ala Ile Gln	
140 145 150 155	
gac atc tcc gtg gaa gag acc tcg gcc aag gaa ggg ctc ctt ctc tgg	590
Asp Ile Ser Val Glu Glu Thr Ser Ala Lys Glu Gly Leu Leu Leu Trp	
160 165 170	
tgc cag aga aag aca gcc cca tat aag aac gtc aat gtg cag aac ttc	638
Cys Gln Arg Lys Thr Ala Pro Tyr Lys Asn Val Asn Val Gln Asn Phe	
175 180 185	
cac atc agc tgg aag gat ggt ctt gcc ttc aat gcc ctg atc cac cgg	686
His Ile Ser Trp Lys Asp Gly Leu Ala Phe Asn Ala Leu Ile His Arg	
190 195 200	
cac aga cca gag ctg att gag tat gac aag ctg agg aag gac gac cct	734
His Arg Pro Glu Leu Ile Glu Tyr Asp Lys Leu Arg Lys Asp Asp Pro	
205 210 215	
gtc acc aac ctg aac aat gcc ttc gaa gtg gct gag aaa tac ctc gac	782
Val Thr Asn Leu Asn Asn Ala Phe Glu Val Ala Glu Lys Tyr Leu Asp	

1241.22

220	225	230	235	
atc ccc aag atg ctg gat gca gag gac atc gtg aac acg gcc cgg ccc	830			
Ile Pro Lys Met Leu Asp Ala Glu Asp Ile Val Asn Thr Ala Arg Pro				
240	245	250		
gac gag aag gcc ata atg acc tat gtg tcc agc ttc tac cat gcc ttt	878			
Asp Glu Lys Ala Ile Met Thr Tyr Val Ser Ser Phe Tyr His Ala Phe				
255	260	265		
tca gga gcg cag aag gct gaa act gaa act gcc gcc aac cgg atc tgt	926			
Ser Gly Ala Gln Lys Ala Glu Thr Glu Thr Ala Ala Asn Arg Ile Cys				
270	275	280		
aag gtg ctg gct gtc aac caa gag aac tgc agc acc tcg atg gag gac	974			
Lys Val Leu Ala Val Asn Gln Glu Asn Cys Ser Thr Ser Met Glu Asp				
285	290	295		
tac gag aag ctg gcc agc gac ctc ctg gag tgg atc cgg cgc acc atc	1022			
Tyr Glu Lys Leu Ala Ser Asp Leu Leu Glu Trp Ile Arg Arg Thr Ile				
300	305	310	315	
ccc tgg ctg gag gac cgt gtg ccc caa aag act atc cag gag atg cag	1070			
Pro Trp Leu Glu Asp Arg Val Pro Gln Lys Thr Ile Gln Glu Met Gln				
320	325	330		
cag aag ctg gag gac ttc cgc gac tac cgg cgt gtg cac aag ccg ccc	1118			
Gln Lys Leu Glu Asp Phe Arg Asp Tyr Arg Arg Val His Lys Pro Pro				
335	340	345		
aag gtg cag gag aag tgc cag ctg gag atc aac ttc aac agc gtg cag	1166			
Lys Val Gln Glu Lys Cys Gln Leu Glu Ile Asn Phe Asn Ser Val Gln				
350	355	360		
acc aag ctg cgc ctc agc aac cgg ccc gcc ttc atg ccc tcc gag ggc	1214			
Thr Lys Leu Arg Leu Ser Asn Arg Pro Ala Phe Met Pro Ser Glu Gly				
365	370	375		
aag atg gtc tcg gac atc aac aat ggc tgg cag cac ttg gag cag gct	1262			
Lys Met Val Ser Asp Ile Asn Asn Gly Trp Gln His Leu Glu Gln Ala				
380	385	390	395	

1241.22

gag aag ggc tac gag gag tgg ctg ctg aat gag att cgc agg ctg gag	1310
Glu Lys Gly Tyr Glu Glu Trp Leu Leu Asn Glu Ile Arg Arg Leu Glu	
400 405 410	
cgg ctc gac cac ctg gca gag aag ttc cgg cag aaa gcc tcc atc cac	1358
Arg Leu Asp His Leu Ala Glu Lys Phe Arg Gln Lys Ala Ser Ile His	
415 420 425	
gag gcc tgg act gac ggg aag gaa gcc atg ctg aag cac cgg gac tac	1406
Glu Ala Trp Thr Asp Gly Lys Glu Ala Met Leu Lys His Arg Asp Tyr	
430 435 440	
gag acg gcc aca cta tcg gac atc aaa gcc ctc att cgc aag cac gag	1454
Glu Thr Ala Thr Leu Ser Asp Ile Lys Ala Leu Ile Arg Lys His Glu	
445 450 455	
gcc ttc gag agc gac ctg gct gcg cac cag gac cgc gtg gag cag atc	1502
Ala Phe Glu Ser Asp Leu Ala Ala His Gln Asp Arg Val Glu Gln Ile	
460 465 470 475	
gcc gcc tcc gcc cag gag ctc aac gag ctg gat tac tac gac tcc cac	1550
Ala Ala Ser Ala Gln Glu Leu Asn Glu Leu Asp Tyr Tyr Asp Ser His	
480 485 490	
aat gtc aac acc cgg tgc cag aag atc tgt gac cag tgg gac gcc ctc	1598
Asn Val Asn Thr Arg Cys Gln Lys Ile Cys Asp Gln Trp Asp Ala Leu	
495 500 505	
ggc tct ctg aca cat agt cgc agg gaa gcc ctg gag aaa aca gag aag	1646
Gly Ser Leu Thr His Ser Arg Arg Glu Ala Leu Glu Lys Thr Glu Lys	
510 515 520	
cag ctg gag gcc atc atc gac cag ctg cac ctg gaa tac gcc aag ccc	1694
Gln Leu Glu Ala Ile Ile Asp Gln Leu His Leu Glu Tyr Ala Lys Pro	
525 530 535	
gcg gcc ccc ttc aac aac tgg atg gag agc gcc atg gag gac ctc cag	1742
Ala Ala Pro Phe Asn Asn Trp Met Glu Ser Ala Met Glu Asp Leu Gln	
540 545 550 555	
gac atg ttc atc gtc cat acc atc gag gag att gag ggc ctg atc tca	1790
Asp Met Phe Ile Val His Thr Ile Glu Glu Ile Glu Gly Leu Ile Ser	

1241.22

560	565	570	
gcc cat gac cag ttc aag tcc acc ctg ccg gac gcc gat agg gag cgc	1838		
Ala His Asp Gln Phe Lys Ser Thr Leu Pro Asp Ala Asp Arg Glu Arg			
575	580	585	
gag gcc atc ctg cat cca caa gga ggc cag agg atc gct gag agc aac	1886		
Glu Ala Ile Leu His Pro Gln Gly Gly Gln Arg Ile Ala Glu Ser Asn			
590	595	600	
cac atc aag ctg tcg ggc agc aac ccc tac acc acc gtc acc ccg caa	1934		
His Ile Lys Leu Ser Gly Ser Asn Pro Tyr Thr Thr Val Thr Pro Gln			
605	610	615	
atc atc aac tcc aag tgg gag aag gtg cag cag ctg gtg cca aaa cgg	1982		
Ile Ile Asn Ser Lys Trp Glu Lys Val Gln Gln Leu Val Pro Lys Arg			
620	625	630	635
gac cat gcc ctc ctg gag gag cag agc aag cag cag cag tcc aac gag	2030		
Asp His Ala Leu Leu Glu Glu Gln Ser Lys Gln Gln Gln Ser Asn Glu			
640	645	650	
cac ctg cgc cgc cag ttc gcc agc cag gcc aat gtt gtg ggg ccc tgg	2078		
His Leu Arg Arg Gln Phe Ala Ser Gln Ala Asn Val Val Gly Pro Trp			
655	660	665	
atc cag acc aag atg gag gag atc gcg atc tcc att gag atg aac ggg	2126		
Ile Gln Thr Lys Met Glu Glu Ile Ala Ile Ser Ile Glu Met Asn Gly			
670	675	680	
acc ctg gag gac cag ctg agc cac ctg aag cag tat gaa cgc agc atc	2174		
Thr Leu Glu Asp Gln Leu Ser His Leu Lys Gln Tyr Glu Arg Ser Ile			
685	690	695	
gtg gac tac aag ccc aac ctg gac ctg ctg gag cag cag cac cag ctc	2222		
Val Asp Tyr Lys Pro Asn Leu Asp Leu Leu Glu Gln Gln His Gln Leu			
700	705	710	715
atc cag gag gcc ctc atc ttc gac aac aag cac acc aac tat acc atg	2270		
Ile Gln Glu Ala Leu Ile Phe Asp Asn Lys His Thr Asn Tyr Thr Met			
720	725	730	

1241.22

gag cac atc cgc gtg ggc tgg gag cag ctg ctc acc acc att gcc cgc	2318
Glu His Ile Arg Val Gly Trp Glu Gln Leu Leu Thr Thr Ile Ala Arg	
735 740 745	
acc atc aac gag gtg gag aac cag atc ctt acc cgc gac gcc aag ggc	2366
Thr Ile Asn Glu Val Glu Asn Gln Ile Leu Thr Arg Asp Ala Lys Gly	
750 755 760	
atc agc cag gag cag atg cag gag ttc cgg gcg tcc ttc aac cac ttc	2414
Ile Ser Gln Glu Gln Met Gln Glu Phe Arg Ala Ser Phe Asn His Phe	
765 770 775	
gac aag gat cat ggc ggg gcg ctg ggg cga gga gtt caa ggc ctg cct	2462
Asp Lys Asp His Gly Gly Ala Leu Gly Arg Gly Val Gln Gly Leu Pro	
780 785 790 795	
cat cag cct ggg cta cga cgt gga gaa cga ccg gca ggt gag gcc gag	2510
His Gln Pro Gly Leu Arg Arg Gly Glu Arg Pro Ala Gly Glu Ala Glu	
800 805 810	
ttc aac cgc atc atg agc ctg gtc gac ccc aac cat agc ggc ctt gtt	2558
Phe Asn Arg Ile Met Ser Leu Val Asp Pro Asn His Ser Gly Leu Val	
815 820 825	
acc ttc caa gcc ttc atc gac ttc atg tcg cgg gag acc acc gac acc	2606
Thr Phe Gln Ala Phe Ile Asp Phe Met Ser Arg Glu Thr Thr Asp Thr	
830 835 840	
gac acg gct gac cag gta atc act tcc ttc aag gtc cta gca ggg gac	2654
Asp Thr Ala Asp Gln Val Ile Thr Ser Phe Lys Val Leu Ala Gly Asp	
845 850 855	
aag aac ttc atc aca gct gag gag ctg cgg aga gag ctg ccc ccc gac	2702
Lys Asn Phe Ile Thr Ala Glu Glu Leu Arg Arg Glu Leu Pro Pro Asp	
860 865 870 875	
cag gcc gag tac tgc atc gcc cgc atg gcg cca tac cag ggc cct gac	2750
Gln Ala Glu Tyr Cys Ile Ala Arg Met Ala Pro Tyr Gln Gly Pro Asp	
880 885 890	
ggc gtg cgc ggt gcc ctc gac tac aag tcc ttc tcc acg gcc ttg tat	2798
Gly Val Arg Gly Ala Leu Asp Tyr Lys Ser Phe Ser Thr Ala Leu Tyr	

1241.22

895

900

905

ggc gag agc gac ctg tgaggcccca gagacctgac ccaacacccc cgacgcctcc 2853

Gly Glu Ser Asp Leu

910

aggagcctgg cagccccaca gtcccatgcc tccactctgt atctatgcaa agcactctct 2913

ctgcagtctc cggggtgggt ggggtgggcag ggaggggctg gggcaggctc tctcctctct 2973

ctctttgtgg gttggccagg aggttcccc gaccagggtg gggagacttg gggccagcgc 3033

ttctggtctg gtaaatatgt atgatgtgtt gtgctttttt aaccaaggag gggccagtgg 3093

attccacag cacaaccggt cccttccatg ccctgggatg cctcaccaca ccagggtctc 3153

ttcctttgct ctgagggtccc ttcaaggcct cccaatcca ggccaaagcc ccatgtgcct 3213

tgtccaggga actgcctggg ccatgcgagg ggccagcaga gggcgccacc acctgacggc 3273

tgggaccac ccagcccctc tcccctctct gctccagact cacttgccat tgccaggaga 3333

tggccccaac aagcaccctg cttttgcagc agaggagctg agttggcaga ccgggcccc 3393

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atcttctaag aaccaaaaaa a 3474

<210> 42

<211> 912

<212> PRT

<213> Homo sapiens

<400> 42

Met Val Asp Tyr His Ala Ala Asn Gln Ser Tyr Gln Tyr Gly Pro Ser

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Ser Ala Ala Met Ala Trp Arg Arg Gly Ser Met Gly Asp Tyr Met Ala

20 25 30

Gln Glu Asp Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp Glu

35 40 45

Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Ser Asn Ser His Leu Arg

50 55 60

Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp Glu Asp Phe Arg Asp Gly

65 70 75 80

Leu Lys Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu Pro

1241.22

	85	90	95
Lys Pro Glu Arg Gly Lys Met Arg Val His Lys Ile Asn Asn Val Asn			
	100	105	110
Lys Ala Leu Asp Phe Ile Ala Ser Lys Gly Ile Lys Leu Asp Phe His			
	115	120	125
Arg Ala Glu Glu Ile Val Asp Gly Asn Ala Lys Met Thr Leu Gly Met			
	130	135	140
Ile Trp Thr Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val Glu			
145	150	155	160
Glu Thr Ser Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys Thr			
	165	170	175
Ala Pro Tyr Lys Asn Val Asn Val Gln Asn Phe His Ile Ser Trp Lys			
	180	185	190
Asp Gly Leu Ala Phe Asn Ala Leu Ile His Arg His Arg Pro Glu Leu			
	195	200	205
Ile Glu Tyr Asp Lys Leu Arg Lys Asp Asp Pro Val Thr Asn Leu Asn			
	210	215	220
Asn Ala Phe Glu Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met Leu			
225	230	235	240
Asp Ala Glu Asp Ile Val Asn Thr Ala Arg Pro Asp Glu Lys Ala Ile			
	245	250	255
Met Thr Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln Lys			
	260	265	270
Ala Glu Thr Glu Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val			
	275	280	285
Asn Gln Glu Asn Cys Ser Thr Ser Met Glu Asp Tyr Glu Lys Leu Ala			
	290	295	300
Ser Asp Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asp			
305	310	315	320
Arg Val Pro Gln Lys Thr Ile Gln Glu Met Gln Gln Lys Leu Glu Asp			
	325	330	335

1241.22

Phe Arg Asp Tyr Arg Arg Val His Lys Pro Pro Lys Val Gln Glu Lys
340 345 350

Cys Gln Leu Glu Ile Asn Phe Asn Ser Val Gln Thr Lys Leu Arg Leu
355 360 365

Ser Asn Arg Pro Ala Phe Met Pro Ser Glu Gly Lys Met Val Ser Asp
370 375 380

Ile Asn Asn Gly Trp Gln His Leu Glu Gln Ala Glu Lys Gly Tyr Glu
385 390 395 400

Glu Trp Leu Leu Asn Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu
405 410 415

Ala Glu Lys Phe Arg Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp
420 425 430

Gly Lys Glu Ala Met Leu Lys His Arg Asp Tyr Glu Thr Ala Thr Leu
435 440 445

Ser Asp Ile Lys Ala Leu Ile Arg Lys His Glu Ala Phe Glu Ser Asp
450 455 460

Leu Ala Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala Ser Ala Gln
465 470 475 480

Glu Leu Asn Glu Leu Asp Tyr Tyr Asp Ser His Asn Val Asn Thr Arg
485 490 495

Cys Gln Lys Ile Cys Asp Gln Trp Asp Ala Leu Gly Ser Leu Thr His
500 505 510

Ser Arg Arg Glu Ala Leu Glu Lys Thr Glu Lys Gln Leu Glu Ala Ile
515 520 525

Ile Asp Gln Leu His Leu Glu Tyr Ala Lys Pro Ala Ala Pro Phe Asn
530 535 540

Asn Trp Met Glu Ser Ala Met Glu Asp Leu Gln Asp Met Phe Ile Val
545 550 555 560

His Thr Ile Glu Glu Ile Glu Gly Leu Ile Ser Ala His Asp Gln Phe
565 570 575

Lys Ser Thr Leu Pro Asp Ala Asp Arg Glu Arg Glu Ala Ile Leu His
580 585 590

1241.22

Pro Gln Gly Gly Gln Arg Ile Ala Glu Ser Asn His Ile Lys Leu Ser
595 600 605
Gly Ser Asn Pro Tyr Thr Thr Val Thr Pro Gln Ile Ile Asn Ser Lys
610 615 620
Trp Glu Lys Val Gln Gln Leu Val Pro Lys Arg Asp His Ala Leu Leu
625 630 635 640
Glu Glu Gln Ser Lys Gln Gln Gln Ser Asn Glu His Leu Arg Arg Gln
645 650 655
Phe Ala Ser Gln Ala Asn Val Val Gly Pro Trp Ile Gln Thr Lys Met
660 665 670
Glu Glu Ile Ala Ile Ser Ile Glu Met Asn Gly Thr Leu Glu Asp Gln
675 680 685
Leu Ser His Leu Lys Gln Tyr Glu Arg Ser Ile Val Asp Tyr Lys Pro
690 695 700
Asn Leu Asp Leu Leu Glu Gln Gln His Gln Leu Ile Gln Glu Ala Leu
705 710 715 720
Ile Phe Asp Asn Lys His Thr Asn Tyr Thr Met Glu His Ile Arg Val
725 730 735
Gly Trp Glu Gln Leu Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val
740 745 750
Glu Asn Gln Ile Leu Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln
755 760 765
Met Gln Glu Phe Arg Ala Ser Phe Asn His Phe Asp Lys Asp His Gly
770 775 780
Gly Ala Leu Gly Arg Gly Val Gln Gly Leu Pro His Gln Pro Gly Leu
785 790 795 800
Arg Arg Gly Glu Arg Pro Ala Gly Glu Ala Glu Phe Asn Arg Ile Met
805 810 815
Ser Leu Val Asp Pro Asn His Ser Gly Leu Val Thr Phe Gln Ala Phe
820 825 830
Ile Asp Phe Met Ser Arg Glu Thr Thr Asp Thr Asp Thr Ala Asp Gln

1241.22

835	840	845	
Val Ile Thr Ser Phe Lys Val	Leu Ala Gly Asp Lys Asn Phe Ile Thr		
850	855	860	
Ala Glu Glu Leu Arg Arg Glu Leu Pro Pro Asp Gln Ala Glu Tyr Cys			
865	870	875	880
Ile Ala Arg Met Ala Pro Tyr Gln Gly Pro Asp Gly Val Arg Gly Ala			
	885	890	895
Leu Asp Tyr Lys Ser Phe Ser Thr Ala Leu Tyr Gly Glu Ser Asp Leu			
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<212> DNA

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Met Pro Ser

1

acg gag aag gac ctg gcg gag gac gcg ccg tgg aag aag atc cag cag 166

Thr Glu Lys Asp Leu Ala Glu Asp Ala Pro Trp Lys Lys Ile Gln Gln

5

10

15

aac aca ttc acg cgc tgg tgc aat gag cac ctc aag tgc gtg ggc aag 214

Asn Thr Phe Thr Arg Trp Cys Asn Glu His Leu Lys Cys Val Gly Lys

20

25

30

35

cgc ctg acc gac ctg cag cgc gac ctc agc gac ggg ctc cgg ctc atc 262

Arg Leu Thr Asp Leu Gln Arg Asp Leu Ser Asp Gly Leu Arg Leu Ile

40

45

50

gcg ctg ctc gag gtg ctc agc cag aag cgc atg tac cgc aag ttc cat 310

1241.22

Ala	Leu	Leu	Glu	Val	Leu	Ser	Gln	Lys	Arg	Met	Tyr	Arg	Lys	Phe	His	
			55					60						65		
ccg	cgc	ccc	aac	ttc	cgc	caa	atg	aag	ctg	gag	aac	gtg	tcc	gtg	gcc	358
Pro	Arg	Pro	Asn	Phe	Arg	Gln	Met	Lys	Leu	Glu	Asn	Val	Ser	Val	Ala	
			70					75						80		
ctc	gag	ttc	ctc	gag	cgc	gag	cac	atc	aag	ctc	gtg	tcc	ata	gac	agc	406
Leu	Glu	Phe	Leu	Glu	Arg	Glu	His	Ile	Lys	Leu	Val	Ser	Ile	Asp	Ser	
			85					90						95		
aag	gcc	atc	gtg	gat	ggg	aac	ctg	aag	ctg	atc	ctg	ggc	ctg	atc	tgg	454
Lys	Ala	Ile	Val	Asp	Gly	Asn	Leu	Lys	Leu	Ile	Leu	Gly	Leu	Ile	Trp	
100					105					110					115	
acg	ctg	atc	ctg	cac	tac	tcc	atc	tcc	atg	ccc	atg	tgg	gag	gat	gaa	502
Thr	Leu	Ile	Leu	His	Tyr	Ser	Ile	Ser	Met	Pro	Met	Trp	Glu	Asp	Glu	
					120					125					130	
gat	gat	gag	gat	gcc	cgc	aaa	cag	acg	ccc	aag	cag	cgg	ctg	ctt	ggc	550
Asp	Asp	Glu	Asp	Ala	Arg	Lys	Gln	Thr	Pro	Lys	Gln	Arg	Leu	Leu	Gly	
				135						140					145	
tgg	atc	cag	aac	aag	gtg	ccc	cag	ctg	ccc	atc	acc	aac	ttc	aac	cgt	598
Trp	Ile	Gln	Asn	Lys	Val	Pro	Gln	Leu	Pro	Ile	Thr	Asn	Phe	Asn	Arg	
				150						155					160	
gac	tgg	cag	gac	ggc	aaa	gct	ctg	ggc	gcc	ctg	gtg	gac	aac	tgc	gcc	646
Asp	Trp	Gln	Asp	Gly	Lys	Ala	Leu	Gly	Ala	Leu	Val	Asp	Asn	Cys	Ala	
				165						170					175	
ccc	ggt	ctc	tgc	ccc	gac	tgg	gag	gcc	tgg	gat	ccc	aac	cag	ccc	gtg	694
Pro	Gly	Leu	Cys	Pro	Asp	Trp	Glu	Ala	Trp	Asp	Pro	Asn	Gln	Pro	Val	
180					185					190					195	
gag	aac	tcc	cgg	gag	gcc	atg	cag	cag	gcc	gac	gac	tgg	ctt	ggg	gtg	742
Glu	Asn	Ser	Arg	Glu	Ala	Met	Gln	Gln	Ala	Asp	Asp	Trp	Leu	Gly	Val	
					200					205					210	
ccc	cag	gtc	att	gcc	cct	gag	gag	att	gtg	gac	ccc	aac	gtg	gat	gag	790
Pro	Gln	Val	Ile	Ala	Pro	Glu	Glu	Ile	Val	Asp	Pro	Asn	Val	Asp	Glu	
				215						220					225	

1241.22

cat tct gtt atg acc tac ctg tcc cag ttc ccc aag gcc aag ctc aaa	838
His Ser Val Met Thr Tyr Leu Ser Gln Phe Pro Lys Ala Lys Leu Lys	
230 235 240	
cct ggt gcc cct gtt cga tcc aag cag ctg aac ccc aag aaa gcc atc	886
Pro Gly Ala Pro Val Arg Ser Lys Gln Leu Asn Pro Lys Lys Ala Ile	
245 250 255	
gcc tat ggg cct ggc atc gag cca cag ggc aac acc gtg ctg cag cct	934
Ala Tyr Gly Pro Gly Ile Glu Pro Gln Gly Asn Thr Val Leu Gln Pro	
260 265 270 275	
gcc cac ttc acc gtg cag acg gtg gac gcg ggc gtg ggc gag gtg ctg	982
Ala His Phe Thr Val Gln Thr Val Asp Ala Gly Val Gly Glu Val Leu	
280 285 290	
gtc tac atc gag gac cct gaa ggc cac acc gag gag gct aag gtg gtt	1030
Val Tyr Ile Glu Asp Pro Glu Gly His Thr Glu Glu Ala Lys Val Val	
295 300 305	
ccc aac aat gac aag gat cgc acc tat gct gtc tcc tat gtg ccc aag	1078
Pro Asn Asn Asp Lys Asp Arg Thr Tyr Ala Val Ser Tyr Val Pro Lys	
310 315 320	
gtc gct ggg tta cac aag gtg acc gtg ctc ttt gct ggc cag aac att	1126
Val Ala Gly Leu His Lys Val Thr Val Leu Phe Ala Gly Gln Asn Ile	
325 330 335	
gaa cgc agt ccc ttt gag gtg aac gtg ggc atg gcc ctg gga gat gcc	1174
Glu Arg Ser Pro Phe Glu Val Asn Val Gly Met Ala Leu Gly Asp Ala	
340 345 350 355	
aac aag gtg tca gcc cgt ggc cct ggc ctg gaa cct gtg ggc aat gtg	1222
Asn Lys Val Ser Ala Arg Gly Pro Gly Leu Glu Pro Val Gly Asn Val	
360 365 370	
gcc aac aaa ccc acc tac ttt gac atc tac act gcg ggc gcc ggc act	1270
Ala Asn Lys Pro Thr Tyr Phe Asp Ile Tyr Thr Ala Gly Ala Gly Thr	
375 380 385	
ggc gat gtt gct gtg gtg atc gtg gac cca cag ggc cgg cgg gac aca	1318

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Gly Asp Val Ala Val Val Ile Val Asp Pro Gln Gly Arg Arg Asp Thr	
390 395 400	
gtg gag gtg gcc ctg gag gac aag ggt gac agc acg ttc cgc tgc aca	1366
Val Glu Val Ala Leu Glu Asp Lys Gly Asp Ser Thr Phe Arg Cys Thr	
405 410 415	
tac aga cct gcc atg gag ggg cca cat acc gtg cat gtg gcc ttt gcg	1414
Tyr Arg Pro Ala Met Glu Gly Pro His Thr Val His Val Ala Phe Ala	
420 425 430 435	
ggg gcc ccc atc acc cgc agt ccc ttc cct gtc cat gtg tcg gaa gcc	1462
Gly Ala Pro Ile Thr Arg Ser Pro Phe Pro Val His Val Ser Glu Ala	
440 445 450	
tgt aac ccc aac gcc tgc cgc gcc tct ggg cga ggc ctg cag ccc aag	1510
Cys Asn Pro Asn Ala Cys Arg Ala Ser Gly Arg Gly Leu Gln Pro Lys	
455 460 465	
ggg gtt cgc gtg aaa gag gtg gct gac ttc aag gtg ttt acc aag ggt	1558
Gly Val Arg Val Lys Glu Val Ala Asp Phe Lys Val Phe Thr Lys Gly	
470 475 480	
gcc ggc agc ggg gag ctc aag gtc acg gtc aag ggg cca aag ggc aca	1606
Ala Gly Ser Gly Glu Leu Lys Val Thr Val Lys Gly Pro Lys Gly Thr	
485 490 495	
gag gag cca gtg aag gtg cgg gag gct ggg gat ggt gtg ttc gag tgc	1654
Glu Glu Pro Val Lys Val Arg Glu Ala Gly Asp Gly Val Phe Glu Cys	
500 505 510 515	
gag tac tac ccg gtg gtg cct ggg aag tat gtg gtg acc atc acg tgg	1702
Glu Tyr Tyr Pro Val Val Pro Gly Lys Tyr Val Val Thr Ile Thr Trp	
520 525 530	
ggc ggc tac gcc atc cct cgc agc ccc ttt gag gta cag gtg agc cca	1750
Gly Gly Tyr Ala Ile Pro Arg Ser Pro Phe Glu Val Gln Val Ser Pro	
535 540 545	
gag gca gga gtg caa aag gtc cgg gcc tgg ggt cct ggt ttg gag act	1798
Glu Ala Gly Val Gln Lys Val Arg Ala Trp Gly Pro Gly Leu Glu Thr	
550 555 560	

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ggc cag gtg ggc aag tca gcc gat ttt gtg gtg gaa gcc att ggc acc	1846
Gly Gln Val Gly Lys Ser Ala Asp Phe Val Val Glu Ala Ile Gly Thr	
565 570 575	
gag gtg ggg aca ctg ggc ttc tcc atc gag ggg ccc tca caa gcc aag	1894
Glu Val Gly Thr Leu Gly Phe Ser Ile Glu Gly Pro Ser Gln Ala Lys	
580 585 590 595	
atc gaa tgt gac gat aag ggg gat ggc tcc tgc gat gtg cgg tac tgg	1942
Ile Glu Cys Asp Asp Lys Gly Asp Gly Ser Cys Asp Val Arg Tyr Trp	
600 605 610	
ccc acg gag cct ggg gag tac gct gtg cac gtc atc tgt gac gat gag	1990
Pro Thr Glu Pro Gly Glu Tyr Ala Val His Val Ile Cys Asp Asp Glu	
615 620 625	
gac atc cga gac tca ccc ttc att gcc cac atc ctg ccc gcc cca cct	2038
Asp Ile Arg Asp Ser Pro Phe Ile Ala His Ile Leu Pro Ala Pro Pro	
630 635 640	
gac tgc ttc cca gat aag gtg aag gcc ttt ggg cct ggc ctg gag cct	2086
Asp Cys Phe Pro Asp Lys Val Lys Ala Phe Gly Pro Gly Leu Glu Pro	
645 650 655	
acc ggc tgc atc gtg gac aag ccc gct gag ttc acc att gat gct cgt	2134
Thr Gly Cys Ile Val Asp Lys Pro Ala Glu Phe Thr Ile Asp Ala Arg	
660 665 670 675	
gca gct ggc aag gga gac ctg aag ctc tat gcc cag gac gcc gac ggc	2182
Ala Ala Gly Lys Gly Asp Leu Lys Leu Tyr Ala Gln Asp Ala Asp Gly	
680 685 690	
tgt ccc atc gac atc aag gtg atc ccc aac ggc aac ggc acc ttc cgc	2230
Cys Pro Ile Asp Ile Lys Val Ile Pro Asn Gly Asn Gly Thr Phe Arg	
695 700 705	
tgc tcc tac gtg ccc acc aag ccc att aag cac acc atc atc atc tcc	2278
Cys Ser Tyr Val Pro Thr Lys Pro Ile Lys His Thr Ile Ile Ile Ser	
710 715 720	
tgg gga ggc gta aac gtg ccc aag agc ccc ttc cgg gtg aac gtg ggc	2326

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atc ata gac aac cat gac tac tcc tac act gtc aag tac acc gct gtc	2854
Ile Ile Asp Asn His Asp Tyr Ser Tyr Thr Val Lys Tyr Thr Ala Val	
900 905 910 915	
cag cag ggc aac atg gca gtg aca gtg act tat ggc ggg gac cct gtc	2902
Gln Gln Gly Asn Met Ala Val Thr Val Thr Tyr Gly Gly Asp Pro Val	
920 925 930	
ccc aag agc ccc ttt gtg gtg aat gtg gca ccc ccg ctg gac ctc agc	2950
Pro Lys Ser Pro Phe Val Val Asn Val Ala Pro Pro Leu Asp Leu Ser	
935 940 945	
aaa atc aaa gtt cag ggc ctt aat agc aag gtg gct gtg gga cag gaa	2998
Lys Ile Lys Val Gln Gly Leu Asn Ser Lys Val Ala Val Gly Gln Glu	
950 955 960	
caa gca ttc tct gtg aac aca cga ggg gct ggc ggt cag ggc caa ctg	3046
Gln Ala Phe Ser Val Asn Thr Arg Gly Ala Gly Gly Gln Gly Gln Leu	
965 970 975	
gat gtg cgg atg act tcg ccc tct cgc cgg ccc atc ccc tgc aag ctg	3094
Asp Val Arg Met Thr Ser Pro Ser Arg Arg Pro Ile Pro Cys Lys Leu	
980 985 990 995	
gag cca ggc ggt gga gcg gaa gcc cag gct gtg cgc tac atg ccc ccg	3142
Glu Pro Gly Gly Gly Ala Glu Ala Gln Ala Val Arg Tyr Met Pro Pro	
1000 1005 1010	
gag gag ggg ccc tac aag gtg gat atc acc tac gat ggt cac ccg gtg	3190
Glu Glu Gly Pro Tyr Lys Val Asp Ile Thr Tyr Asp Gly His Pro Val	
1015 1020 1025	
cct ggc agc ccg ttt gct gtg gag ggt gtc ctg ccc cct gat ccc tcc	3238
Pro Gly Ser Pro Phe Ala Val Glu Gly Val Leu Pro Pro Asp Pro Ser	
1030 1035 1040	
aag gtc tgt gct tat ggc ccg ggt ctc aag ggt gga ctg gta ggc acc	3286
Lys Val Cys Ala Tyr Gly Pro Gly Leu Lys Gly Gly Leu Val Gly Thr	
1045 1050 1055	
ccc gcg cca ttc tcc atc gac acc aag ggg gct ggc aca ggt ggc ctg	3334

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Pro Ala Pro Phe Ser Ile Asp Thr Lys Gly Ala Gly Thr Gly Gly Leu	
1060	1065 1070 1075
ggg ctg acc gta gag ggc ccc tgc gag gcc aag atc gag tgc cag gac	3382
Gly Leu Thr Val Glu Gly Pro Cys Glu Ala Lys Ile Glu Cys Gln Asp	
	1080 1085 1090
aat ggt gat ggc tca tgt gct gtc agc tac ctg ccc acg gag cct ggc	3430
Asn Gly Asp Gly Ser Cys Ala Val Ser Tyr Leu Pro Thr Glu Pro Gly	
	1095 1100 1105
gag tac acc atc aac atc ctg ttt gct gag gcc cac atc cct ggc tcg	3478
Glu Tyr Thr Ile Asn Ile Leu Phe Ala Glu Ala His Ile Pro Gly Ser	
	1110 1115 1120
ccc ttc aaa gcc acc att cgg cct gtg ttt gac ccg agc aag gtg cgg	3526
Pro Phe Lys Ala Thr Ile Arg Pro Val Phe Asp Pro Ser Lys Val Arg	
	1125 1130 1135
gcc agt gga ccg ggc ctg gag cgc ggc aag gtc ggt gag gca gcc acc	3574
Ala Ser Gly Pro Gly Leu Glu Arg Gly Lys Val Gly Glu Ala Ala Thr	
	1140 1145 1150 1155
ttc act gtg gac tgc tca gag gca ggc gag gcg gag ctg acc att gag	3622
Phe Thr Val Asp Cys Ser Glu Ala Gly Glu Ala Glu Leu Thr Ile Glu	
	1160 1165 1170
atc ctg tcg gat gcc ggg gtc aag gcc gag gtg ctg atc cac aac aac	3670
Ile Leu Ser Asp Ala Gly Val Lys Ala Glu Val Leu Ile His Asn Asn	
	1175 1180 1185
gcg gat ggc acc tac cac atc acc tac agc cct gcc ttc cct ggc acc	3718
Ala Asp Gly Thr Tyr His Ile Thr Tyr Ser Pro Ala Phe Pro Gly Thr	
	1190 1195 1200
tac acc att acc atc aag tat ggc ggg cat ccc gtg ccc aaa ttc ccc	3766
Tyr Thr Ile Thr Ile Lys Tyr Gly Gly His Pro Val Pro Lys Phe Pro	
	1205 1210 1215
acc cgt gtc cat gtg cag cct gcg gtc gat acc agt ggc gtc aag gtc	3814
Thr Arg Val His Val Gln Pro Ala Val Asp Thr Ser Gly Val Lys Val	
1220	1225 1230 1235

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tca ggg cct ggt gtt gag cca cac ggt gtc ctg cgg gag gtg acc act	3862
Ser Gly Pro Gly Val Glu Pro His Gly Val Leu Arg Glu Val Thr Thr	
1240 1245 1250	
gag ttc act gtg gat gca aga tcc cta aca gcc aca ggc ggc aac cac	3910
Glu Phe Thr Val Asp Ala Arg Ser Leu Thr Ala Thr Gly Gly Asn His	
1255 1260 1265	
gtg acg gct cgt gtg ctc aac ccc tcg ggg gcc aag aca gac acc tat	3958
Val Thr Ala Arg Val Leu Asn Pro Ser Gly Ala Lys Thr Asp Thr Tyr	
1270 1275 1280	
gtg aca gac aat ggg gac ggc acc tac cga gtg cag tac acc gcc tac	4006
Val Thr Asp Asn Gly Asp Gly Thr Tyr Arg Val Gln Tyr Thr Ala Tyr	
1285 1290 1295	
gag gag ggc gtg cat ctg gtg gag gtc ctg tat gat gag gtc gct gtg	4054
Glu Glu Gly Val His Leu Val Glu Val Leu Tyr Asp Glu Val Ala Val	
1300 1305 1310 1315	
ccc aag agc ccc ttc cga gtg ggc gtg acc gag ggc tgt gat ccc acc	4102
Pro Lys Ser Pro Phe Arg Val Gly Val Thr Glu Gly Cys Asp Pro Thr	
1320 1325 1330	
cgc gtc cga gcc ttc ggg cca ggc ctg gag ggt ggc ttg gtc aac aag	4150
Arg Val Arg Ala Phe Gly Pro Gly Leu Glu Gly Gly Leu Val Asn Lys	
1335 1340 1345	
gcc aac cga ttc act gtg gag acc agg gga gcg ggc acc ggg ggc ctt	4198
Ala Asn Arg Phe Thr Val Glu Thr Arg Gly Ala Gly Thr Gly Gly Leu	
1350 1355 1360	
ggc cta gcc atc gag ggt ccc tcg gaa gcc aag atg tcc tgc aag gac	4246
Gly Leu Ala Ile Glu Gly Pro Ser Glu Ala Lys Met Ser Cys Lys Asp	
1365 1370 1375	
aac aag gat ggt agc tgc acc gtg gag tac atc ccc ttc act cct gga	4294
Asn Lys Asp Gly Ser Cys Thr Val Glu Tyr Ile Pro Phe Thr Pro Gly	
1380 1385 1390 1395	
gac tat gac gtc aac atc acc ttc ggg ggg cgg ccc atc cca ggg agc	4342

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Asp Tyr Asp Val Asn Ile Thr Phe Gly Gly Arg Pro Ile Pro Gly Ser	
1400	1405
ccg ttc cgc gtg cca gtg aag gat gtg gtg gac cct ggg aag gtg aag	4390
Pro Phe Arg Val Pro Val Lys Asp Val Val Asp Pro Gly Lys Val Lys	
1415	1420
tgc tca ggg cca ggg ctg ggg gct ggt gtc agg gcc cgg gtt cct cag	4438
Cys Ser Gly Pro Gly Leu Gly Ala Gly Val Arg Ala Arg Val Pro Gln	
1430	1435
acc ttc aca gtg gac tgc agt caa gct ggc cgg gcg ccc ctg cag gtg	4486
Thr Phe Thr Val Asp Cys Ser Gln Ala Gly Arg Ala Pro Leu Gln Val	
1445	1450
gct gtg ctg ggc ccc aca ggt gtg gcc gag cct gtg gag gtg cgg gac	4534
Ala Val Leu Gly Pro Thr Gly Val Ala Glu Pro Val Glu Val Arg Asp	
1460	1465
aat gga gat ggc acc cac act gtc cac tac acc cca gcc act gac ggg	4582
Asn Gly Asp Gly Thr His Thr Val His Tyr Thr Pro Ala Thr Asp Gly	
1480	1485
ccc tac acg gta gcc gtc aag tat gct gac cag gag gtg cca cgc agc	4630
Pro Tyr Thr Val Ala Val Lys Tyr Ala Asp Gln Glu Val Pro Arg Ser	
1495	1500
ccc ttc aag atc aag gtc ctc cca gct cat gat gcc agc aag gtg cgg	4678
Pro Phe Lys Ile Lys Val Leu Pro Ala His Asp Ala Ser Lys Val Arg	
1510	1515
gcc agc ggg cca ggc ctc aac gcc tct ggc atc cct gcc agc ctg cct	4726
Ala Ser Gly Pro Gly Leu Asn Ala Ser Gly Ile Pro Ala Ser Leu Pro	
1525	1530
gtg gag ttc acc atc gac gca cgg gac gcg ggc gag ggg ttg ctc act	4774
Val Glu Phe Thr Ile Asp Ala Arg Asp Ala Gly Glu Gly Leu Leu Thr	
1540	1545
gtc cag atc ttg ggc ccc gag ggt aag ccc aag aag gcc aac atc cgg	4822
Val Gln Ile Leu Gly Pro Glu Gly Lys Pro Lys Lys Ala Asn Ile Arg	
1560	1565
	1570

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gac aat ggg gat ggc acg tac gct gtg tcc tac ctg ccg gac atg agt	4870
Asp Asn Gly Asp Gly Thr Tyr Ala Val Ser Tyr Leu Pro Asp Met Ser	
1575 1580 1585	
ggc cgg tac acc atc acc atc aag tat ggc ggt gat gag atc ccc tac	4918
Gly Arg Tyr Thr Ile Thr Ile Lys Tyr Gly Gly Asp Glu Ile Pro Tyr	
1590 1595 1600	
tcg ccc ttc cgc atc cat gct ctg ccc act ggg gat gcc agc aag tgc	4966
Ser Pro Phe Arg Ile His Ala Leu Pro Thr Gly Asp Ala Ser Lys Cys	
1605 1610 1615	
ctc gtc aca gtg tcc att gga ggc cat ggc ctg ggt gcc tgc ctg ggc	5014
Leu Val Thr Val Ser Ile Gly Gly His Gly Leu Gly Ala Cys Leu Gly	
1620 1625 1630 1635	
cct cga atc cag att ggg cag gag acg gtg atc acg gtg gat gcc aag	5062
Pro Arg Ile Gln Ile Gly Gln Glu Thr Val Ile Thr Val Asp Ala Lys	
1640 1645 1650	
gca gcc ggt gag ggg aag gtg aca tgc acg gtg tcc acg ccg gat ggg	5110
Ala Ala Gly Glu Gly Lys Val Thr Cys Thr Val Ser Thr Pro Asp Gly	
1655 1660 1665	
gca gag ctc gat gtg gat gtg gtt gag aac cat gac ggt acc ttt gac	5158
Ala Glu Leu Asp Val Asp Val Val Glu Asn His Asp Gly Thr Phe Asp	
1670 1675 1680	
atc tac tac aca gcg ccc gag ccg ggc aag tac gtc atc acc atc cgc	5206
Ile Tyr Tyr Thr Ala Pro Glu Pro Gly Lys Tyr Val Ile Thr Ile Arg	
1685 1690 1695	
ttc ggg ggt gag cac atc ccc aac agc ccc ttc cac gtg ctg gcg tgt	5254
Phe Gly Gly Glu His Ile Pro Asn Ser Pro Phe His Val Leu Ala Cys	
1700 1705 1710 1715	
gac ccc ctg ccg cac gag gag gag ccc tct gaa gtg cca cag ctg cgc	5302
Asp Pro Leu Pro His Glu Glu Glu Pro Ser Glu Val Pro Gln Leu Arg	
1720 1725 1730	
cag ccc tac gct cct ccc cgg ccc ggc gcc cgc ccc aca cac tgg gcc	5350

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Gln Pro Tyr Ala Pro Pro Arg Pro Gly Ala Arg Pro Thr His Trp Ala	
1735	1740 1745
aca gag gag cca gtg gtg cct gtg gag cca atg gag tcc atg ctg agg	5398
Thr Glu Glu Pro Val Val Pro Val Glu Pro Met Glu Ser Met Leu Arg	
1750	1755 1760
ccc ttc aac ctg gtc atc ccc ttc gcg gtg cag aaa ggg gag ctc aca	5446
Pro Phe Asn Leu Val Ile Pro Phe Ala Val Gln Lys Gly Glu Leu Thr	
1765	1770 1775
gga gag gtg cgg atg ccc tcg ggg aag acg gca cgg ccc aac atc acc	5494
Gly Glu Val Arg Met Pro Ser Gly Lys Thr Ala Arg Pro Asn Ile Thr	
1780	1785 1790 1795
gac aac aag gac ggc acc atc acg gtg agg tat gca ccc act gag aaa	5542
Asp Asn Lys Asp Gly Thr Ile Thr Val Arg Tyr Ala Pro Thr Glu Lys	
1800	1805 1810
ggc ctg cac cag atg ggg atc aag tat gac ggc aac cac atc cct ggg	5590
Gly Leu His Gln Met Gly Ile Lys Tyr Asp Gly Asn His Ile Pro Gly	
1815	1820 1825
agc ccc tta cag ttc tat gtg gat gcc atc aac agc cgc cat gtc agt	5638
Ser Pro Leu Gln Phe Tyr Val Asp Ala Ile Asn Ser Arg His Val Ser	
1830	1835 1840
gcc tat ggg cca ggc ctg agc cat ggc atg gtc aac aag cca gcc acc	5686
Ala Tyr Gly Pro Gly Leu Ser His Gly Met Val Asn Lys Pro Ala Thr	
1845	1850 1855
ttc act att gtc acc aaa gat gct gga gaa ggg ggt ctg tca ctg gcc	5734
Phe Thr Ile Val Thr Lys Asp Ala Gly Glu Gly Gly Leu Ser Leu Ala	
1860	1865 1870 1875
gtg gag ggc cca tcc aag gca gag atc acc tgt aag gac aac aag gat	5782
Val Glu Gly Pro Ser Lys Ala Glu Ile Thr Cys Lys Asp Asn Lys Asp	
1880	1885 1890
ggc acc tgc acc gtg tcc tat ctg ccg act gcg cct gga gac tac agc	5830
Gly Thr Cys Thr Val Ser Tyr Leu Pro Thr Ala Pro Gly Asp Tyr Ser	
1895	1900 1905

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atc atc gtg cgc ttc gat gac aag cac atc ccg ggg agc ccc ttc aca	5878
Ile Ile Val Arg Phe Asp Asp Lys His Ile Pro Gly Ser Pro Phe Thr	
1910 1915 1920	
gcc aag atc aca ggt gat gac tcc atg agg acc tca cag ctg aat gtg	5926
Ala Lys Ile Thr Gly Asp Asp Ser Met Arg Thr Ser Gln Leu Asn Val	
1925 1930 1935	
ggc acc tcc acg gac gtg tca ctg aag atc acc gag agt gat ctg agc	5974
Gly Thr Ser Thr Asp Val Ser Leu Lys Ile Thr Glu Ser Asp Leu Ser	
1940 1945 1950 1955	
cag ctg acc gcc agc atc cgt gcc ccc tcg ggc aac gag gag ccc tgc	6022
Gln Leu Thr Ala Ser Ile Arg Ala Pro Ser Gly Asn Glu Glu Pro Cys	
1960 1965 1970	
ctg ctg aag cgc ctg ccc aac cgg cac att ggg atc tcc ttc acc ccc	6070
Leu Leu Lys Arg Leu Pro Asn Arg His Ile Gly Ile Ser Phe Thr Pro	
1975 1980 1985	
aag gag gtc ggg gag cac gtg gtg agc gtg cgc aag agt ggc aag cat	6118
Lys Glu Val Gly Glu His Val Val Ser Val Arg Lys Ser Gly Lys His	
1990 1995 2000	
gtc acc aac agc ccc ttc aag atc ctg gtg ggg cca tct gag atc ggg	6166
Val Thr Asn Ser Pro Phe Lys Ile Leu Val Gly Pro Ser Glu Ile Gly	
2005 2010 2015	
gac gcc agc aag gtg cgg gtc tgg ggc aag ggg ctt tcc gag gga cac	6214
Asp Ala Ser Lys Val Arg Val Trp Gly Lys Gly Leu Ser Glu Gly His	
2020 2025 2030 2035	
aca ttc cag gtg gca gag ttc atc gtg gac act cgc aat gca ggt tat	6262
Thr Phe Gln Val Ala Glu Phe Ile Val Asp Thr Arg Asn Ala Gly Tyr	
2040 2045 2050	
ggg ggc ttg ggg ctg agt att gaa ggc cca agc aag gtg gac atc aac	6310
Gly Gly Leu Gly Leu Ser Ile Glu Gly Pro Ser Lys Val Asp Ile Asn	
2055 2060 2065	
tgt gag gac atg gag gac ggg aca tgc aaa gtc acc tac tgc ccc acc	6358

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Cys Glu Asp Met Glu Asp Gly Thr Cys Lys Val Thr Tyr Cys Pro Thr	
2070	2075
2080	
gag ccc ggc acc tac atc atc aac atc aag ttt gct gac aag cac gtg	6406
Glu Pro Gly Thr Tyr Ile Ile Asn Ile Lys Phe Ala Asp Lys His Val	
2085	2090
2095	
cct gga agc ccc ttc act gtg aag gtg acc ggc gag ggc cgc atg aag	6454
Pro Gly Ser Pro Phe Thr Val Lys Val Thr Gly Glu Gly Arg Met Lys	
2100	2105
2110	2115
gag agc atc acc cgg cgg aga cag gca cct tcc atc gcc acc atc ggc	6502
Glu Ser Ile Thr Arg Arg Arg Gln Ala Pro Ser Ile Ala Thr Ile Gly	
2120	2125
2130	
agc acc tgt gac ctc aac ctc aag atc cca gga aac tgg ttc cag atg	6550
Ser Thr Cys Asp Leu Asn Leu Lys Ile Pro Gly Asn Trp Phe Gln Met	
2135	2140
2145	
gtg tct gcc cag gag cgc ctg aca cgc acc ttc aca cgc agc agc cac	6598
Val Ser Ala Gln Glu Arg Leu Thr Arg Thr Phe Thr Arg Ser Ser His	
2150	2155
2160	
acc tac acc cgc acg gag cgc acg gag atc agc aag acg cgg ggc ggg	6646
Thr Tyr Thr Arg Thr Glu Arg Thr Glu Ile Ser Lys Thr Arg Gly Gly	
2165	2170
2175	
gag aca aag ccc gag gtg cgg gtg gag gag tcc acc cag gtc ggc ggg	6694
Glu Thr Lys Pro Glu Val Arg Val Glu Glu Ser Thr Gln Val Gly Gly	
2180	2185
2190	2195
gac ccc ttc cct gct gtg ttt ggg gac ttc ctg ggc cgg gag cgc ctg	6742
Asp Pro Phe Pro Ala Val Phe Gly Asp Phe Leu Gly Arg Glu Arg Leu	
2200	2205
2210	
gga tcc ttc ggc agc atc acc cgg cag cag gag ggt gag gcc agc tct	6790
Gly Ser Phe Gly Ser Ile Thr Arg Gln Gln Glu Gly Glu Ala Ser Ser	
2215	2220
2225	
cag gac atg act gca cag gtg acc agc cca tcg ggc aag gtg gaa gcc	6838
Gln Asp Met Thr Ala Gln Val Thr Ser Pro Ser Gly Lys Val Glu Ala	
2230	2235
2240	

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gca gag atc gtc gag ggc gag gac agc gcc tac agc gtc cgc ttt gtg	6886
Ala Glu Ile Val Glu Gly Glu Asp Ser Ala Tyr Ser Val Arg Phe Val	
2245 2250 2255	
ccc cag gaa atg ggg ccc cat acg gtc gct gtc aag tac cgt ggc cag	6934
Pro Gln Glu Met Gly Pro His Thr Val Ala Val Lys Tyr Arg Gly Gln	
2260 2265 2270 2275	
cac gtg ccc ggc agc ccc ttt cag ttc act gtg ggg ccg ctg ggt gaa	6982
His Val Pro Gly Ser Pro Phe Gln Phe Thr Val Gly Pro Leu Gly Glu	
2280 2285 2290	
ggg ggt gcc cac aag gtg cgg gcc gga cga gca ggg ctg gag cga ggt	7030
Gly Gly Ala His Lys Val Arg Ala Gly Arg Ala Gly Leu Glu Arg Gly	
2295 2300 2305	
gtg gcc ggc gtg cca gcc gag ttc agc atc tgg acc cgg gag gct ggc	7078
Val Ala Gly Val Pro Ala Glu Phe Ser Ile Trp Thr Arg Glu Ala Gly	
2310 2315 2320	
gct ggg ggc ctg tcc att gct gtg gag ggt cct agc aaa gcg gag att	7126
Ala Gly Gly Leu Ser Ile Ala Val Glu Gly Pro Ser Lys Ala Glu Ile	
2325 2330 2335	
gca ttt gag gat cgc aaa gat ggc tcc tgc ggc gtc tcc tat gtc gtc	7174
Ala Phe Glu Asp Arg Lys Asp Gly Ser Cys Gly Val Ser Tyr Val Val	
2340 2345 2350 2355	
cag gaa cca ggt gac tat gag gtc tcc atc aag ttc aat gat gag cac	7222
Gln Glu Pro Gly Asp Tyr Glu Val Ser Ile Lys Phe Asn Asp Glu His	
2360 2365 2370	
atc cca gac agc ccc ttt gtg gtg cct gtg gcc tcc ctc tcg gat gac	7270
Ile Pro Asp Ser Pro Phe Val Val Pro Val Ala Ser Leu Ser Asp Asp	
2375 2380 2385	
gct cgc cgt ctc act gtc acc agc ctc cag gag acg ggg ctc aag gtg	7318
Ala Arg Arg Leu Thr Val Thr Ser Leu Gln Glu Thr Gly Leu Lys Val	
2390 2395 2400	
aac cag cca gcg tcc ttt gcc gtg cag ctg aac ggt gcc cgg ggc gtg	7366

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ggc cac agc ctt cac gaa aca tcc acg gtt ctg gtg gag act gtg acc	7894
Gly His Ser Leu His Glu Thr Ser Thr Val Leu Val Glu Thr Val Thr	
2580 2585 2590 2595	
aag tcc tcc tca agc cgg ggc tcc agc tac agc tcc atc ccc aag ttc	7942
Lys Ser Ser Ser Ser Arg Gly Ser Ser Tyr Ser Ser Ile Pro Lys Phe	
2600 2605 2610	
tcc tca gat gcc agc aag gtg gtg act cgg ggc cct ggg ctg tcc cag	7990
Ser Ser Asp Ala Ser Lys Val Val Thr Arg Gly Pro Gly Leu Ser Gln	
2615 2620 2625	
gcc ttc gtg ggc cag aag aac tcc ttc acc gtg gac tgc agc aaa gca	8038
Ala Phe Val Gly Gln Lys Asn Ser Phe Thr Val Asp Cys Ser Lys Ala	
2630 2635 2640	
ggc acc aac atg atg atg gtg ggc gtg cac ggc ccc aag acc ccc tgt	8086
Gly Thr Asn Met Met Met Val Gly Val His Gly Pro Lys Thr Pro Cys	
2645 2650 2655	
gag gag gtg tac gtg aag cac atg ggg aac cgg gtg tac aat gtc acc	8134
Glu Glu Val Tyr Val Lys His Met Gly Asn Arg Val Tyr Asn Val Thr	
2660 2665 2670 2675	
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Tyr Thr Val Lys Glu Lys Gly Asp Tyr Ile Leu Ile Val Lys Trp Gly	
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Asp Glu Ser Val Pro Gly Ser Pro Phe Lys Val Lys Val Pro	
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Arg	Leu	Ile	Ala	Leu	Leu	Glu	Val	Leu	Ser	Gln	Lys	Arg	Met	Tyr	Arg
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Lys	Phe	His	Pro	Arg	Pro	Asn	Phe	Arg	Gln	Met	Lys	Leu	Glu	Asn	Val
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Ser	Val	Ala	Leu	Glu	Phe	Leu	Glu	Arg	Glu	His	Ile	Lys	Leu	Val	Ser
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Leu Gly Val Pro Gln Val Ile Ala Pro Glu Glu Ile Val Asp Pro Asn
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Val Asp Glu His Ser Val Met Thr Tyr Leu Ser Gln Phe Pro Lys Ala
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Lys Leu Lys Pro Gly Ala Pro Val Arg Ser Lys Gln Leu Asn Pro Lys
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Lys Ala Ile Ala Tyr Gly Pro Gly Ile Glu Pro Gln Gly Asn Thr Val
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Glu Val Leu Val Tyr Ile Glu Asp Pro Glu Gly His Thr Glu Glu Ala
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Val Pro Lys Val Ala Gly Leu His Lys Val Thr Val Leu Phe Ala Gly
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Gly Asp Ala Asn Lys Val Ser Ala Arg Gly Pro Gly Leu Glu Pro Val
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Gly Asn Val Ala Asn Lys Pro Thr Tyr Phe Asp Ile Tyr Thr Ala Gly
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Ala Gly Thr Gly Asp Val Ala Val Val Ile Val Asp Pro Gln Gly Arg
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Arg Asp Thr Val Glu Val Ala Leu Glu Asp Lys Gly Asp Ser Thr Phe
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Ser Glu Ala Cys Asn Pro Asn Ala Cys Arg Ala Ser Gly Arg Gly Leu
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Gln Pro Lys Gly Val Arg Val Lys Glu Val Ala Asp Phe Lys Val Phe
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Ile Gly Thr Glu Val Gly Thr Leu Gly Phe Ser Ile Glu Gly Pro Ser
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Gln Ala Lys Ile Glu Cys Asp Asp Lys Gly Asp Gly Ser Cys Asp Val
595 600 605
Arg Tyr Trp Pro Thr Glu Pro Gly Glu Tyr Ala Val His Val Ile Cys
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Asp Asp Glu Asp Ile Arg Asp Ser Pro Phe Ile Ala His Ile Leu Pro
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Ala Pro Pro Asp Cys Phe Pro Asp Lys Val Lys Ala Phe Gly Pro Gly
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Leu Glu Pro Thr Gly Cys Ile Val Asp Lys Pro Ala Glu Phe Thr Ile

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 Pro Ala Ser Pro Phe His Ile Lys Val Asp Pro Ser His Asp Ala Ser
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 Thr Ala Val Gln Gln Gly Asn Met Ala Val Thr Val Thr Tyr Gly Gly

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Asp Leu Ser Lys Ile Lys Val Gln Gly Leu Asn Ser Lys Val Ala Val			
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Gly Gln Glu Gln Ala Phe Ser Val Asn Thr Arg Gly Ala Gly Gly Gln			
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Gly Gln Leu Asp Val Arg Met Thr Ser Pro Ser Arg Arg Pro Ile Pro			
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Cys Lys Leu Glu Pro Gly Gly Gly Ala Glu Ala Gln Ala Val Arg Tyr			
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Met Pro Pro Glu Glu Gly Pro Tyr Lys Val Asp Ile Thr Tyr Asp Gly			
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His Pro Val Pro Gly Ser Pro Phe Ala Val Glu Gly Val Leu Pro Pro			
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Asp Pro Ser Lys Val Cys Ala Tyr Gly Pro Gly Leu Lys Gly Gly Leu			
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Val Gly Thr Pro Ala Pro Phe Ser Ile Asp Thr Lys Gly Ala Gly Thr			
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Cys Gln Asp Asn Gly Asp Gly Ser Cys Ala Val Ser Tyr Leu Pro Thr			
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Pro Gly Thr Tyr Thr Ile Thr Ile Lys Tyr Gly Gly His Pro Val Pro
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Val Lys Val Ser Gly Pro Gly Val Glu Pro His Gly Val Leu Arg Glu
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Val Thr Thr Glu Phe Thr Val Asp Ala Arg Ser Leu Thr Ala Thr Gly
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Gly Asn His Val Thr Ala Arg Val Leu Asn Pro Ser Gly Ala Lys Thr
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Asp Thr Tyr Val Thr Asp Asn Gly Asp Gly Thr Tyr Arg Val Gln Tyr
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Gly Gly Leu Gly Leu Ala Ile Glu Gly Pro Ser Glu Ala Lys Met Ser
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Pro Asp Gly Ala Glu Leu Asp Val Asp Val Val Glu Asn His Asp Gly

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Pro Ala Thr Phe Thr Ile Val Thr Lys Asp Ala Gly Glu Gly Gly Leu			
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Ser Leu Ala Val Glu Gly Pro Ser Lys Ala Glu Ile Thr Cys Lys Asp			
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Glu Pro Cys Leu Leu Lys Arg Leu Pro Asn Arg His Ile Gly Ile Ser			
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Glu Ile Gly Asp Ala Ser Lys Val Arg Val Trp Gly Lys Gly Leu Ser			
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Glu Gly His Thr Phe Gln Val Ala Glu Phe Ile Val Asp Thr Arg Asn			
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Ala Gly Tyr Gly Gly Leu Gly Leu Ser Ile Glu Gly Pro Ser Lys Val			
	2050	2055	2060
Asp Ile Asn Cys Glu Asp Met Glu Asp Gly Thr Cys Lys Val Thr Tyr			
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Cys Pro Thr Glu Pro Gly Thr Tyr Ile Ile Asn Ile Lys Phe Ala Asp			
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Phe Gln Met Val Ser Ala Gln Glu Arg Leu Thr Arg Thr Phe Thr Arg			
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Ser Ser His Thr Tyr Thr Arg Thr Glu Arg Thr Glu Ile Ser Lys Thr			
	2165	2170	2175

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Ala Ser Ser Gln Asp Met Thr Ala Gln Val Thr Ser Pro Ser Gly Lys		
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Val Glu Ala Ala Glu Ile Val Glu Gly Glu Asp Ser Ala Tyr Ser Val		
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Arg Gly Gln His Val Pro Gly Ser Pro Phe Gln Phe Thr Val Gly Pro		
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Tyr Val Val Gln Glu Pro Gly Asp Tyr Glu Val Ser Ile Lys Phe Asn		
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Asp Glu His Ile Pro Asp Ser Pro Phe Val Val Pro Val Ala Ser Leu		
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Leu Lys Val Asn Gln Pro Ala Ser Phe Ala Val Gln Leu Asn Gly Ala		
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Arg Gly Val Ile Asp Ala Arg Val His Thr Pro Ser Gly Ala Val Glu		
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Pro Met Ala Pro Gly Asn Tyr Leu Ile Ala Ile Lys Tyr Gly Gly Pro
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<211> 381

<212> PRT

<213> Homo sapiens

<400> 46

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His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys
      20             25             30
Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp
      35             40             45
Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
      50             55             60
Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
      65             70             75             80
Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
      85             90             95
Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
      100            105            110
Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val
      115            120            125
Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
      130            135            140

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<211> 2743

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (240)..(2387)

<400> 47

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tagggccgcg gccgggcccc gccacgcgcg cacacgcccc tcgatgactt tcctccgggg 120
cgcgcgggcg tgagcccggg gcgagggctg tcttcccga gacccgaccc cggcagcgcg 180
gggcggccac ttctcctgtg cctccgcccc ctgctccact ccccgccgcc gccgcgcgg 239
atg cca agc acc agc ttt cca gtc cct tcc aag ttt cca ctt ggc cct 287
Met Pro Ser Thr Ser Phe Pro Val Pro Ser Lys Phe Pro Leu Gly Pro
      1              5              10              15
gcg gct gcg gtc ttc ggg aga gga gaa act ttg ggg ccc gcg ccg cgc 335
Ala Ala Ala Val Phe Gly Arg Gly Glu Thr Leu Gly Pro Ala Pro Arg
              20              25              30
gcc ggc ggc acc atg aag tca gcg gag gaa gaa cac tat ggc tat gca 383
Ala Gly Gly Thr Met Lys Ser Ala Glu Glu Glu His Tyr Gly Tyr Ala
              35              40              45
tcc tcc aac gtc agc ccc gcc ctg ccg ctc ccc acg gcg cac tcc acc 431
Ser Ser Asn Val Ser Pro Ala Leu Pro Leu Pro Thr Ala His Ser Thr
              50              55              60
ctg ccg gcc ccg tgc cac aac ctt cag acc tcc aca ccg ggc atc atc 479
Leu Pro Ala Pro Cys His Asn Leu Gln Thr Ser Thr Pro Gly Ile Ile
              65              70              75              80
ccg ccg gcg gat cac ccc tcg ggg tac gga gca gct ttg gac ggt ggg 527
Pro Pro Ala Asp His Pro Ser Gly Tyr Gly Ala Ala Leu Asp Gly Gly
              85              90              95
ccc gcg ggc tac ttc ctc tcc tcc ggc cac acc agg cct gat ggg gcc 575
Pro Ala Gly Tyr Phe Leu Ser Ser Gly His Thr Arg Pro Asp Gly Ala
              100              105              110

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1241.22

cct gcc ctg gag agt cct cgc atc gag ata acc tcg tgc ttg ggc ctg	623
Pro Ala Leu Glu Ser Pro Arg Ile Glu Ile Thr Ser Cys Leu Gly Leu	
115 120 125	
tac cac aac aat aac cag ttt ttc cac gat gtg gag gtg gaa gac gtc	671
Tyr His Asn Asn Asn Gln Phe Phe His Asp Val Glu Val Glu Asp Val	
130 135 140	
ctc cct agc tcc aaa cgg tcc ccc tcc acg gcc acg ctg agt ctg ccc	719
Leu Pro Ser Ser Lys Arg Ser Pro Ser Thr Ala Thr Leu Ser Leu Pro	
145 150 155 160	
agc ctg gag gcc tac aga gac ccc tcg tgc ctg agc ccg gcc agc agc	767
Ser Leu Glu Ala Tyr Arg Asp Pro Ser Cys Leu Ser Pro Ala Ser Ser	
165 170 175	
ctg tcc tcc cgg agc tgc aac tca gag gcc tcc tcc tac gag tcc aac	815
Leu Ser Ser Arg Ser Cys Asn Ser Glu Ala Ser Ser Tyr Glu Ser Asn	
180 185 190	
tac tcg tac ccg tac gcg tcc ccc cag acg tcg cca tgg cag tct ccc	863
Tyr Ser Tyr Pro Tyr Ala Ser Pro Gln Thr Ser Pro Trp Gln Ser Pro	
195 200 205	
tgc gtg tct ccc aag acc acg gac ccc gag gag ggc ttt ccc cgc ggg	911
Cys Val Ser Pro Lys Thr Thr Asp Pro Glu Glu Gly Phe Pro Arg Gly	
210 215 220	
ctg ggg gcc tgc aca ctg ctg ggt tcc ccg cag cac tcc ccc tcc acc	959
Leu Gly Ala Cys Thr Leu Leu Gly Ser Pro Gln His Ser Pro Ser Thr	
225 230 235 240	
tcg ccc cgc gcc agc gtc act gag gag agc tgg ctg ggt gcc cgc tcc	1007
Ser Pro Arg Ala Ser Val Thr Glu Glu Ser Trp Leu Gly Ala Arg Ser	
245 250 255	
tcc aga ccc gcg tcc cct tgc aac aag agg aag tac agc ctc aac ggc	1055
Ser Arg Pro Ala Ser Pro Cys Asn Lys Arg Lys Tyr Ser Leu Asn Gly	
260 265 270	
cgg cag ccg ccc tac tca ccc cac cac tcg ccc acg ccg tcc ccg cac	1103

1241.22

Arg	Gln	Pro	Pro	Tyr	Ser	Pro	His	His	Ser	Pro	Thr	Pro	Ser	Pro	His		
				275					280					285			
ggc	tcc	ccg	cgg	gtc	agc	gtg	acc	gac	gac	tcg	tgg	ttg	ggc	aac	acc	1151	
Gly	Ser	Pro	Arg	Val	Ser	Val	Thr	Asp	Asp	Ser	Trp	Leu	Gly	Asn	Thr		
				290					295					300			
acc	cag	tac	acc	agc	tcg	gcc	atc	gtg	gcc	gcc	atc	aac	gcg	ctg	acc	1199	
Thr	Gln	Tyr	Thr	Ser	Ser	Ala	Ile	Val	Ala	Ala	Ile	Asn	Ala	Leu	Thr		
				305					310					315			
acc	gac	agc	agc	ctg	gac	ctg	gga	gat	ggc	gtc	cct	gtc	aag	tcc	cgc	1247	
Thr	Asp	Ser	Ser	Leu	Asp	Leu	Gly	Asp	Gly	Val	Pro	Val	Lys	Ser	Arg		
				325					330					335			
aag	acc	acc	ctg	gag	cag	ccg	ccc	tca	gtg	gcg	ctc	aag	gtg	gag	ccc	1295	
Lys	Thr	Thr	Leu	Glu	Gln	Pro	Pro	Ser	Val	Ala	Leu	Lys	Val	Glu	Pro		
				340					345					350			
gtc	ggg	gag	gac	ctg	ggc	agc	ccc	ccg	ccc	ccg	gcc	gac	ttc	gcg	ccc	1343	
Val	Gly	Glu	Asp	Leu	Gly	Ser	Pro	Pro	Pro	Pro	Ala	Asp	Phe	Ala	Pro		
				355					360					365			
gaa	gac	tac	tcc	tct	ttc	cag	cac	atc	agg	aag	ggc	ggc	ttc	tgc	gac	1391	
Glu	Asp	Tyr	Ser	Ser	Phe	Gln	His	Ile	Arg	Lys	Gly	Gly	Phe	Cys	Asp		
				370					375					380			
cag	tac	ctg	gcg	gtg	ccg	cag	cac	ccc	tac	cag	tgg	gcg	aag	ccc	aag	1439	
Gln	Tyr	Leu	Ala	Val	Pro	Gln	His	Pro	Tyr	Gln	Trp	Ala	Lys	Pro	Lys		
				385					390					395			
ccc	ctg	tcc	cct	acg	tcc	tac	atg	agc	ccg	acc	ctg	ccc	gcc	ctg	gac	1487	
Pro	Leu	Ser	Pro	Thr	Ser	Tyr	Met	Ser	Pro	Thr	Leu	Pro	Ala	Leu	Asp		
				405					410					415			
tgg	cag	ctg	ccg	tcc	cac	tca	ggc	ccg	tat	gag	ctt	cgg	att	gag	gtg	1535	
Trp	Gln	Leu	Pro	Ser	His	Ser	Gly	Pro	Tyr	Glu	Leu	Arg	Ile	Glu	Val		
				420					425					430			
cag	ccc	aag	tcc	cac	cac	cga	gcc	cac	tac	gag	acg	gag	ggc	agc	cgg	1583	
Gln	Pro	Lys	Ser	His	His	Arg	Ala	His	Tyr	Glu	Thr	Glu	Gly	Ser	Arg		
				435					440					445			

1241.22

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ggg gcc gtg aag gcg tcg gcc gga gga cac ccc atc gtg cag ctg cat 1631
Gly Ala Val Lys Ala Ser Ala Gly Gly His Pro Ile Val Gln Leu His
    450                455                460

ggc tac ttg gag aat gag ccg ctg atg ctg cag ctt ttc att ggg acg 1679
Gly Tyr Leu Glu Asn Glu Pro Leu Met Leu Gln Leu Phe Ile Gly Thr
465                470                475                480

gcg gac gac cgc ctg ctg cgc ccg cac gcc ttc tac cag gtg cac cgc 1727
Ala Asp Asp Arg Leu Leu Arg Pro His Ala Phe Tyr Gln Val His Arg
    485                490                495

atc aca ggg aag acc gtg tcc acc acc agc cac gag gct atc ctc tcc 1775
Ile Thr Gly Lys Thr Val Ser Thr Thr Ser His Glu Ala Ile Leu Ser
    500                505                510

aac acc aaa gtc ctg gag atc cca ctc ctg ccg gag aac agc atg cga 1823
Asn Thr Lys Val Leu Glu Ile Pro Leu Leu Pro Glu Asn Ser Met Arg
    515                520                525

gcc gtc att gac tgt gcc gga atc ctg aaa ctc aga aac tcc gac att 1871
Ala Val Ile Asp Cys Ala Gly Ile Leu Lys Leu Arg Asn Ser Asp Ile
    530                535                540

gaa ctt cgg aaa gga gag acg gac atc ggg agg aag aac aca cgg gta 1919
Glu Leu Arg Lys Gly Glu Thr Asp Ile Gly Arg Lys Asn Thr Arg Val
545                550                555                560

cgg ctg gtg ttc cgc gtt cac gtc ccg caa ccc agc ggc cgc acg ctg 1967
Arg Leu Val Phe Arg Val His Val Pro Gln Pro Ser Gly Arg Thr Leu
    565                570                575

tcc ctg cag gtg gcc tcc aac ccc atc gaa tgc tcc cag cgc tca gct 2015
Ser Leu Gln Val Ala Ser Asn Pro Ile Glu Cys Ser Gln Arg Ser Ala
    580                585                590

cag gag ctg cct ctg gtg gag aag cag agc acg gac agc tat ccg gtc 2063
Gln Glu Leu Pro Leu Val Glu Lys Gln Ser Thr Asp Ser Tyr Pro Val
    595                600                605

gtg ggc ggg aag aag atg gtc ctg tct ggc cac aac ttc ctg cag gac 2111

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1241.22

Val Gly Gly Lys Lys Met Val Leu Ser Gly His Asn Phe Leu Gln Asp
610 615 620

tcc aag gtc att ttc gtg gag aaa gcc cca gat ggc cac cat gtc tgg 2159
Ser Lys Val Ile Phe Val Glu Lys Ala Pro Asp Gly His His Val Trp
625 630 635 640

gag atg gaa gcg aaa act gac cgg gac ctg tgc aag ccg aat tct ctg 2207
Glu Met Glu Ala Lys Thr Asp Arg Asp Leu Cys Lys Pro Asn Ser Leu
645 650 655

gtg gtt gag atc ccg cca ttt cgg aat cag agg ata acc agc ccc gtt 2255
Val Val Glu Ile Pro Pro Phe Arg Asn Gln Arg Ile Thr Ser Pro Val
660 665 670

cac gtc agt ttc tac gtc tgc aac ggg aag aga aag cga agc cag tac 2303
His Val Ser Phe Tyr Val Cys Asn Gly Lys Arg Lys Arg Ser Gln Tyr
675 680 685

cag cgt ttc acc tac ctt ccc gcc aac ggt aac gcc atc ttt cta acc 2351
Gln Arg Phe Thr Tyr Leu Pro Ala Asn Gly Asn Ala Ile Phe Leu Thr
690 695 700

gta agc cgt gaa cat gag cgc gtg ggg tgc ttt ttc taaagacgca 2397
Val Ser Arg Glu His Glu Arg Val Gly Cys Phe Phe
705 710 715

gaaacgacgt cgccgtaaaag cagcgtggcg tggtgcacat ttaactgtgt gatgtcccgt 2457
tagtgagacc gagccatcga tgccctgaaa aggaaaggaa aagggaagct tcggatgcat 2517
tttccttgat ccctgttggg ggtggggggc ggggggttgca tactcagata gtcacggtta 2577
ttttgcttct tgcgaaatgta taacagccaa ggggaaaaca tggctcttct gctccaaaaa 2637
actgaggggg tcctggtgtg catttgcacc ctaaagctgc ttacggtgaa aaggcaaata 2697
ggtatagcta ttttgcaggc accttagga ataaactttg ctttta 2743

<210> 48

<211> 716

<212> PRT

<213> Homo sapiens

<400> 48

1241.22

Met	Pro	Ser	Thr	Ser	Phe	Pro	Val	Pro	Ser	Lys	Phe	Pro	Leu	Gly	Pro
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Ala	Ala	Ala	Val	Phe	Gly	Arg	Gly	Glu	Thr	Leu	Gly	Pro	Ala	Pro	Arg
			20					25					30		
Ala	Gly	Gly	Thr	Met	Lys	Ser	Ala	Glu	Glu	Glu	His	Tyr	Gly	Tyr	Ala
			35				40					45			
Ser	Ser	Asn	Val	Ser	Pro	Ala	Leu	Pro	Leu	Pro	Thr	Ala	His	Ser	Thr
		50				55					60				
Leu	Pro	Ala	Pro	Cys	His	Asn	Leu	Gln	Thr	Ser	Thr	Pro	Gly	Ile	Ile
65					70					75				80	
Pro	Pro	Ala	Asp	His	Pro	Ser	Gly	Tyr	Gly	Ala	Ala	Leu	Asp	Gly	Gly
				85				90						95	
Pro	Ala	Gly	Tyr	Phe	Leu	Ser	Ser	Gly	His	Thr	Arg	Pro	Asp	Gly	Ala
			100					105						110	
Pro	Ala	Leu	Glu	Ser	Pro	Arg	Ile	Glu	Ile	Thr	Ser	Cys	Leu	Gly	Leu
			115					120						125	
Tyr	His	Asn	Asn	Asn	Gln	Phe	Phe	His	Asp	Val	Glu	Val	Glu	Asp	Val
		130				135								140	
Leu	Pro	Ser	Ser	Lys	Arg	Ser	Pro	Ser	Thr	Ala	Thr	Leu	Ser	Leu	Pro
145					150					155				160	
Ser	Leu	Glu	Ala	Tyr	Arg	Asp	Pro	Ser	Cys	Leu	Ser	Pro	Ala	Ser	Ser
				165						170				175	
Leu	Ser	Ser	Arg	Ser	Cys	Asn	Ser	Glu	Ala	Ser	Ser	Tyr	Glu	Ser	Asn
			180					185						190	
Tyr	Ser	Tyr	Pro	Tyr	Ala	Ser	Pro	Gln	Thr	Ser	Pro	Trp	Gln	Ser	Pro
			195					200						205	
Cys	Val	Ser	Pro	Lys	Thr	Thr	Asp	Pro	Glu	Glu	Gly	Phe	Pro	Arg	Gly
				210										220	
Leu	Gly	Ala	Cys	Thr	Leu	Leu	Gly	Ser	Pro	Gln	His	Ser	Pro	Ser	Thr
225					230					235				240	
Ser	Pro	Arg	Ala	Ser	Val	Thr	Glu	Glu	Ser	Trp	Leu	Gly	Ala	Arg	Ser
				245						250				255	

1241.22

Ser Arg Pro Ala Ser Pro Cys Asn Lys Arg Lys Tyr Ser Leu Asn Gly
260 265 270
Arg Gln Pro Pro Tyr Ser Pro His His Ser Pro Thr Pro Ser Pro His
275 280 285
Gly Ser Pro Arg Val Ser Val Thr Asp Asp Ser Trp Leu Gly Asn Thr
290 295 300
Thr Gln Tyr Thr Ser Ser Ala Ile Val Ala Ala Ile Asn Ala Leu Thr
305 310 315 320
Thr Asp Ser Ser Leu Asp Leu Gly Asp Gly Val Pro Val Lys Ser Arg
325 330 335
Lys Thr Thr Leu Glu Gln Pro Pro Ser Val Ala Leu Lys Val Glu Pro
340 345 350
Val Gly Glu Asp Leu Gly Ser Pro Pro Pro Pro Ala Asp Phe Ala Pro
355 360 365
Glu Asp Tyr Ser Ser Phe Gln His Ile Arg Lys Gly Gly Phe Cys Asp
370 375 380
Gln Tyr Leu Ala Val Pro Gln His Pro Tyr Gln Trp Ala Lys Pro Lys
385 390 395 400
Pro Leu Ser Pro Thr Ser Tyr Met Ser Pro Thr Leu Pro Ala Leu Asp
405 410 415
Trp Gln Leu Pro Ser His Ser Gly Pro Tyr Gln Leu Arg Ile Glu Val
420 425 430
Gln Pro Lys Ser His His Arg Ala His Tyr Glu Thr Glu Gly Ser Arg
435 440 445
Gly Ala Val Lys Ala Ser Ala Gly Gly His Pro Ile Val Gln Leu His
450 455 460
Gly Tyr Leu Glu Asn Glu Pro Leu Met Leu Gln Leu Phe Ile Gly Thr
465 470 475 480
Ala Asp Asp Arg Leu Leu Arg Pro His Ala Phe Tyr Gln Val His Arg
485 490 495
Ile Thr Gly Lys Thr Val Ser Thr Thr Ser His Glu Ala Ile Leu Ser

1241.22

500	505	510
Asn Thr Lys Val Leu Glu Ile Pro Leu Leu Pro Glu Asn Ser Met Arg		
515	520	525
Ala Val Ile Asp Cys Ala Gly Ile Leu Lys Leu Arg Asn Ser Asp Ile		
530	535	540
Glu Leu Arg Lys Gly Glu Thr Asp Ile Gly Arg Lys Asn Thr Arg Val		
545	550	555
Arg Leu Val Phe Arg Val His Val Pro Gln Pro Ser Gly Arg Thr Leu		
565	570	575
Ser Leu Gln Val Ala Ser Asn Pro Ile Glu Cys Ser Gln Arg Ser Ala		
580	585	590
Gln Glu Leu Pro Leu Val Glu Lys Gln Ser Thr Asp Ser Tyr Pro Val		
595	600	605
Val Gly Gly Lys Lys Met Val Leu Ser Gly His Asn Phe Leu Gln Asp		
610	615	620
Ser Lys Val Ile Phe Val Glu Lys Ala Pro Asp Gly His His Val Trp		
625	630	635
Glu Met Glu Ala Lys Thr Asp Arg Asp Leu Cys Lys Pro Asn Ser Leu		
645	650	655
Val Val Glu Ile Pro Pro Phe Arg Asn Gln Arg Ile Thr Ser Pro Val		
660	665	670
His Val Ser Phe Tyr Val Cys Asn Gly Lys Arg Lys Arg Ser Gln Tyr		
675	680	685
Gln Arg Phe Thr Tyr Leu Pro Ala Asn Gly Asn Ala Ile Phe Leu Thr		
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Val Ser Arg Glu His Glu Arg Val Gly Cys Phe Phe		
705	710	715

<210> 49

<211> 2353

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (241)..(1482)

<400> 49

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ccgcccggcc gcagccgagg agccgaggcc gcccgggccg tggcgggcga gccctcagcc 240
atg gcc tcg ggc gac acc ctc tac atc gcc acg gac ggc tcg gag atg 288
Met Ala Ser Gly Asp Thr Leu Tyr Ile Ala Thr Asp Gly Ser Glu Met
      1             5             10             15
ccg gcc gag atc gtg gag ctg cac gag atc gag gtg gag acc atc ccg 336
Pro Ala Glu Ile Val Glu Leu His Glu Ile Glu Val Glu Thr Ile Pro
              20              25              30
gtg gag acc atc gag acc aca gtg gtg ggc gag gag gag gag gag gac 384
Val Glu Thr Ile Glu Thr Thr Val Val Gly Glu Glu Glu Glu Glu Asp
              35              40              45
gac gac gac gag gac ggc ggc ggt ggc gac cac ggc ggc ggc ggc ggc 432
Asp Asp Asp Glu Asp Gly Gly Gly Gly Asp His Gly Gly Gly Gly Gly
              50              55              60
cac ggc cac gcc ggc cac cac cac cac cac cat cac cac cac cac cac 480
His Gly His Ala Gly His His His His His His His His His His His
              65              70              75              80
ccg ccc atg atc gct ctg cag ccg ctg gtc acc gac gac ccg acc cag 528
Pro Pro Met Ile Ala Leu Gln Pro Leu Val Thr Asp Asp Pro Thr Gln
              85              90              95
gtg cac cac cac cag gag gtg atc ctg gtg cag acg cgc gag gag gtg 576
Val His His His Gln Glu Val Ile Leu Val Gln Thr Arg Glu Glu Val
              100             105             110
gtg ggc ggc gac gac tcg gac ggc ctg cgc gcc gag gac ggc ttc gag 624
Val Gly Gly Asp Asp Ser Asp Gly Leu Arg Ala Glu Asp Gly Phe Glu
              115             120             125

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1241.22

gat cag att ctc atc ccg gtg ccc gcg ccg gcc ggc ggc gac gac gac	672
Asp Gln Ile Leu Ile Pro Val Pro Ala Pro Ala Gly Gly Asp Asp Asp	
130 135 140	
tac att gaa caa acg ctg gtc acc gtg gcg gcg gcc ggc aag agc ggc	720
Tyr Ile Glu Gln Thr Leu Val Thr Val Ala Ala Ala Gly Lys Ser Gly	
145 150 155 160	
ggc ggc ggc tcg tcg tcg tcg gga ggc ggc cgc gtc aag aag ggc ggc	768
Gly Gly Gly Ser Ser Ser Ser Gly Gly Gly Arg Val Lys Lys Gly Gly	
165 170 175	
ggc aag aag agc ggc aag aag agt tac ctc agc ggc ggc gcc ggc gcg	816
Gly Lys Lys Ser Gly Lys Lys Ser Tyr Leu Ser Gly Gly Ala Gly Ala	
180 185 190	
gcg ggc ggc cgc ggc gcc gac ccg ggc aac aag aag tgg gag cag aag	864
Ala Gly Gly Arg Gly Ala Asp Pro Gly Asn Lys Lys Trp Glu Gln Lys	
195 200 205	
cag gtg cag atc aag acc ctg gag ggc gag ttc tcg gtc acc atg tgg	912
Gln Val Gln Ile Lys Thr Leu Glu Gly Glu Phe Ser Val Thr Met Trp	
210 215 220	
tcc tca gat gaa aaa aaa gat att gac cat gag aca gtg gtt gaa gaa	960
Ser Ser Asp Glu Lys Lys Asp Ile Asp His Glu Thr Val Val Glu Glu	
225 230 235 240	
cag atc att gga gag aac tca cct cct gat tat tca gaa tat atg aca	1008
Gln Ile Ile Gly Glu Asn Ser Pro Pro Asp Tyr Ser Glu Tyr Met Thr	
245 250 255	
gga aag aaa ctt cct cct gga gga ata cct ggc att gac ctc tca gat	1056
Gly Lys Lys Leu Pro Pro Gly Gly Ile Pro Gly Ile Asp Leu Ser Asp	
260 265 270	
ccc aaa caa ctg gca gaa ttt gct aga atg aag cca aga aaa att aaa	1104
Pro Lys Gln Leu Ala Glu Phe Ala Arg Met Lys Pro Arg Lys Ile Lys	
275 280 285	
gaa gat gat gct cca aga aca ata gct tgc cct cat aaa ggc tgc aca	1152

1241.22

Glu Asp Asp Ala Pro Arg Thr Ile Ala Cys Pro His Lys Gly Cys Thr
290 295 300

aag atg ttc agg gat aac tcg gcc atg aga aaa cat ctg cac acc cac 1200
Lys Met Phe Arg Asp Asn Ser Ala Met Arg Lys His Leu His Thr His
305 310 315 320

ggt ccc aga gtc cac gtc tgt gca gaa tgt ggc aaa gct ttt gtt gag 1248
Gly Pro Arg Val His Val Cys Ala Glu Cys Gly Lys Ala Phe Val Glu
325 330 335

agt tca aaa cta aaa cga cac caa ctg gtt cat act gga gag aag ccc 1296
Ser Ser Lys Leu Lys Arg His Gln Leu Val His Thr Gly Glu Lys Pro
340 345 350

ttt cag tgc acg ttc gaa ggc tgt ggg aaa cgc ttt tca ctg gac ttc 1344
Phe Gln Cys Thr Phe Glu Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe
355 360 365

aat ttg cgc aca cat gtg cga atc cat acc gga gac agg ccc tat gtg 1392
Asn Leu Arg Thr His Val Arg Ile His Thr Gly Asp Arg Pro Tyr Val
370 375 380

tgc ccc ttc gat ggt tgt aat aag aag ttt gct cag tca act aac ctg 1440
Cys Pro Phe Asp Gly Cys Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu
385 390 395 400

aaa tct cac atc tta aca cat gct aag gcc aaa aac aac cag 1482
Lys Ser His Ile Leu Thr His Ala Lys Ala Lys Asn Asn Gln
405 410

tgaaaagaag agagaagacc cttctcgacc acgggaagca tcttcagaa gtgtgattgg 1542
gaataaatat gcctctcctt tgtatattat ttctaggaag aattttaaaa atgaatccta 1602
cacacctaag ggacatgttt tgataaagta gtaaaaatta aaaaaaaaaa actttactaa 1662
gatgacattg ctaagatgct ctatcttgct ctgtaatctc gtttcaaaaa cacagtgttt 1722
ttgtaaagtg tgggtcccaac aggaggacaa ttcatgaact tcgcatcaaa agacaattct 1782
ttatacaaca gtgctaataa tgggacttct ttccacattc ttataaatat gaagctcacc 1842
tgttgcttac aattttttta attttgtatt ttccaagtgt gcatattgta cacttttttg 1902
gggatatgct tagtaatgct acgtgtgatt tttctggagg ttgataactt tgcttgagct 1962
agattttctt taaaagaatg ggcagttaca tgcatacttc aaaagtattt tcctgtaaaa 2022

1241.22

aaaaaaaaag ttatataggt tttgtttgct atcttaattt tggttgtatt ctttgatggt 2082
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atgtgattta atagtgttaa tcaatttaaa cccatttttag tcactttttt tttccaaaaa 2202
aatactgcca gatgctgatg ttcagtgtaa tttctttgcc tgttcagtta cagaaagtgg 2262
tgctcagttg tagaatgtat tgtacctttt aacacctgat gtgtacatcc catgtaacag 2322
aaagggaac aataaaatag caatcctaaa g 2353

<210> 50

<211> 414

<212> PRT

<213> Homo sapiens

<400> 50

Met Ala Ser Gly Asp Thr Leu Tyr Ile Ala Thr Asp Gly Ser Glu Met

1 5 10 15

Pro Ala Glu Ile Val Glu Leu His Glu Ile Glu Val Glu Thr Ile Pro

20 25 30

Val Glu Thr Ile Glu Thr Thr Val Val Gly Glu Glu Glu Glu Asp

35 40 45

Asp Asp Asp Glu Asp Gly Gly Gly Gly Asp His Gly Gly Gly Gly Gly

50 55 60

His Gly His Ala Gly His His His His His His His His His His

65 70 75 80

Pro Pro Met Ile Ala Leu Gln Pro Leu Val Thr Asp Asp Pro Thr Gln

85 90 95

Val His His His Gln Glu Val Ile Leu Val Gln Thr Arg Glu Glu Val

100 105 110

Val Gly Gly Asp Asp Ser Asp Gly Leu Arg Ala Glu Asp Gly Phe Glu

115 120 125

Asp Gln Ile Leu Ile Pro Val Pro Ala Pro Ala Gly Gly Asp Asp Asp

130 135 140

Tyr Ile Glu Gln Thr Leu Val Thr Val Ala Ala Ala Gly Lys Ser Gly

145 150 155 160

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Gly Gly Gly Ser Ser Ser Ser Gly Gly Gly Arg Val Lys Lys Gly Gly
165 170 175
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Ala Gly Gly Arg Gly Ala Asp Pro Gly Asn Lys Lys Trp Glu Gln Lys
195 200 205
Gln Val Gln Ile Lys Thr Leu Glu Gly Glu Phe Ser Val Thr Met Trp
210 215 220
Ser Ser Asp Glu Lys Lys Asp Ile Asp His Glu Thr Val Val Glu Glu
225 230 235 240
Gln Ile Ile Gly Glu Asn Ser Pro Pro Asp Tyr Ser Glu Tyr Met Thr
245 250 255
Gly Lys Lys Leu Pro Pro Gly Gly Ile Pro Gly Ile Asp Leu Ser Asp
260 265 270
Pro Lys Gln Leu Ala Glu Phe Ala Arg Met Lys Pro Arg Lys Ile Lys
275 280 285
Glu Asp Asp Ala Pro Arg Thr Ile Ala Cys Pro His Lys Gly Cys Thr
290 295 300
Lys Met Phe Arg Asp Asn Ser Ala Met Arg Lys His Leu His Thr His
305 310 315 320
Gly Pro Arg Val His Val Cys Ala Glu Cys Gly Lys Ala Phe Val Glu
325 330 335
Ser Ser Lys Leu Lys Arg His Gln Leu Val His Thr Gly Glu Lys Pro
340 345 350
Phe Gln Cys Thr Phe Glu Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe
355 360 365
Asn Leu Arg Thr His Val Arg Ile His Thr Gly Asp Arg Pro Tyr Val
370 375 380
Cys Pro Phe Asp Gly Cys Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu
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Lys Ser His Ile Leu Thr His Ala Lys Ala Lys Asn Asn Gln

405 1241.22
410

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ccaacattac ttgagtcctt ggataaaatt gagaaaagag tctacaagta ttgtggactc 180
tacaggaggc aggaggctga caactggcag taaagacaaa g atg tca ggc ctg cgg 236

Met Ser Gly Leu Arg

1 5

ccc ggc act caa gtg gac cct gag att gag ctt ttt gta aag gct gga 284
Pro Gly Thr Gln Val Asp Pro Glu Ile Glu Leu Phe Val Lys Ala Gly

10 15 20

agt gat gga gag agt att gga aac tgt ccc ttt tgc caa cgc ctt ttc 332
Ser Asp Gly Glu Ser Ile Gly Asn Cys Pro Phe Cys Gln Arg Leu Phe

25 30 35

atg atc ctc tgg ctt aaa gga gtt aaa ttt aat gtg aca act gtt gac 380
Met Ile Leu Trp Leu Lys Gly Val Lys Phe Asn Val Thr Thr Val Asp

40 45 50

atg acc aga aag cct gaa gaa cta aag gac tta gcc cca ggt acc aat 428
Met Thr Arg Lys Pro Glu Glu Leu Lys Asp Leu Ala Pro Gly Thr Asn

55 60 65

cct ccg ttc ctg gtg tat aac aag gag ttg aaa aca gac ttc att aaa 476
Pro Pro Phe Leu Val Tyr Asn Lys Glu Leu Lys Thr Asp Phe Ile Lys

70 75 80 85

att gag gag ttt tta gaa caa acc ctg gct cct cca agg tac cct cac 524

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Ile Glu Glu Phe Leu Glu Gln Thr Leu Ala Pro Pro Arg Tyr Pro His
90 95 100
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Leu Ser Pro Lys Tyr Lys Glu Ser Phe Asp Val Gly Cys Asn Leu Phe
105 110 115
gcc aag ttt tct gca tac att aag aat aca caa aag gag gca aat aag 620
Ala Lys Phe Ser Ala Tyr Ile Lys Asn Thr Gln Lys Glu Ala Asn Lys
120 125 130
aat ttt gaa aaa tct ctg ctc aaa gaa ttc aag cgt ctg gat gac tac 668
Asn Phe Glu Lys Ser Leu Leu Lys Glu Phe Lys Arg Leu Asp Asp Tyr
135 140 145
tta aac acc cca ctt ctg gat gaa att gat cca gac agt gct ggg gaa 716
Leu Asn Thr Pro Leu Leu Asp Glu Ile Asp Pro Asp Ser Ala Gly Glu
150 155 160 165
ccc cca gtt tcc aga aga cta ttc ttg gat ggg gac cag cta aca ctg 764
Pro Pro Val Ser Arg Arg Leu Phe Leu Asp Gly Asp Gln Leu Thr Leu
170 175 180
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Ala Asp Cys Ser Leu Leu Pro Lys Leu Asn Ile Ile Lys Val Ala Ala
185 190 195
aag aaa tat cgt gac ttt gac att cca gca gaa ttc tca gga gtc tgg 860
Lys Lys Tyr Arg Asp Phe Asp Ile Pro Ala Glu Phe Ser Gly Val Trp
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cgt tat ctc cac aat gcc tat gcc cgt gaa gaa ttt acc cac acg tgt 908
Arg Tyr Leu His Asn Ala Tyr Ala Arg Glu Glu Phe Thr His Thr Cys
215 220 225
cct gaa gac aaa gaa att gaa aat act tac gca aat gtg gct 950
Pro Glu Asp Lys Glu Ile Glu Asn Thr Tyr Ala Asn Val Ala
230 235 240
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<210> 52

<211> 243

<212> PRT

<213> Homo sapiens

<400> 52

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20 25 30
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35 40 45
Val Thr Thr Val Asp Met Thr Arg Lys Pro Glu Glu Leu Lys Asp Leu
50 55 60
Ala Pro Gly Thr Asn Pro Pro Phe Leu Val Tyr Asn Lys Glu Leu Lys
65 70 75 80
Thr Asp Phe Ile Lys Ile Glu Glu Phe Leu Glu Gln Thr Leu Ala Pro
85 90 95
Pro Arg Tyr Pro His Leu Ser Pro Lys Tyr Lys Glu Ser Phe Asp Val
100 105 110
Gly Cys Asn Leu Phe Ala Lys Phe Ser Ala Tyr Ile Lys Asn Thr Gln
115 120 125
Lys Glu Ala Asn Lys Asn Phe Glu Lys Ser Leu Leu Lys Glu Phe Lys
130 135 140
Arg Leu Asp Asp Tyr Leu Asn Thr Pro Leu Leu Asp Glu Ile Asp Pro
145 150 155 160
Asp Ser Ala Gly Glu Pro Pro Val Ser Arg Arg Leu Phe Leu Asp Gly
165 170 175
Asp Gln Leu Thr Leu Ala Asp Cys Ser Leu Leu Pro Lys Leu Asn Ile
180 185 190

1241.22

Ile Lys Val Ala Ala Lys Lys Tyr Arg Asp Phe Asp Ile Pro Ala Glu
195 200 205
Phe Ser Gly Val Trp Arg Tyr Leu His Asn Ala Tyr Ala Arg Glu Glu
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<212> DNA

<213> Homo sapiens

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Ile Ala Lys Lys Lys Thr His Val Lys Lys Cys Thr Leu Asn Pro Ile
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Phe Asn Glu Ser Phe Ile Tyr Asp Ile Pro Thr Asp Leu Leu Pro Asp
35 40 45
atc agc atc gag ttc ctc gtt atc gac ttc gat cgc acc acc aag aat 193
Ile Ser Ile Glu Phe Leu Val Ile Asp Phe Asp Arg Thr Thr Lys Asn
50 55 60
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Glu Val Val Gly Arg Leu Ile Leu Gly Ala His Ser Val Thr Ala Ser
65 70 75 80
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Gly Ala Glu His Trp Arg Glu Val Cys Glu Ser Pro Arg Lys Pro Val

85

90

95

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Ala Lys Trp His Ser Leu Ser Glu Tyr

100

105

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aaagctaaca tgaattgtgt gaaattgcat aatgctgtaa tgctaattcta caatatgtaa 3936
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acatt 4001

<210> 54

<211> 105

<212> PRT

<213> Homo sapiens

<400> 54

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Phe Asn Glu Ser Phe Ile Tyr Asp Ile Pro Thr Asp Leu Leu Pro Asp
35 40 45
Ile Ser Ile Glu Phe Leu Val Ile Asp Phe Asp Arg Thr Thr Lys Asn
50 55 60
Glu Val Val Gly Arg Leu Ile Leu Gly Ala His Ser Val Thr Ala Ser
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Gly Ala Glu His Trp Arg Glu Val Cys Glu Ser Pro Arg Lys Pro Val
85 90 95
Ala Lys Trp His Ser Leu Ser Glu Tyr
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<210> 55

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<213> Homo sapiens

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<222> (118)..(909)

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atg gaa tca ggc ttc acc tcc aag gac acc tat cta agc cat ttt aac	165					
Met Glu Ser Gly Phe Thr Ser Lys Asp Thr Tyr Leu Ser His Phe Asn						
1	5	10	15			
cct cgg gat tac cta gaa aaa tat tac aag ttt ggt tct agg cac tct	213					
Pro Arg Asp Tyr Leu Glu Lys Tyr Tyr Lys Phe Gly Ser Arg His Ser						
20	25	30				
gca gaa agc cag att ctt aag cac ctt ctg aaa aat ctt ttc aag ata	261					
Ala Glu Ser Gln Ile Leu Lys His Leu Leu Lys Asn Leu Phe Lys Ile						
35	40	45				
ttc tgc cta gac ggt gtg aag gga gac ctg ctg att gac atc ggc tct	309					
Phe Cys Leu Asp Gly Val Lys Gly Asp Leu Leu Ile Asp Ile Gly Ser						
50	55	60				
ggc ccc act atc tat cag ctc ctc tct gct tgt gaa tcc ttt aag gag	357					
Gly Pro Thr Ile Tyr Gln Leu Leu Ser Ala Cys Glu Ser Phe Lys Glu						
65	70	75	80			
atc gtc gtc act gac tac tca gac cag aac ctg cag gag ctg gag aag	405					
Ile Val Val Thr Asp Tyr Ser Asp Gln Asn Leu Gln Glu Leu Glu Lys						
85	90	95				
tgg ctg aag aaa gag cca gag gcc ttt gac tgg tcc cca gtg gtg acc	453					
Trp Leu Lys Lys Glu Pro Glu Ala Phe Asp Trp Ser Pro Val Val Thr						
100	105	110				
tat gtg tgt gat ctt gaa ggg aac aga gtc aag ggt cca gag aag gag	501					
Tyr Val Cys Asp Leu Glu Gly Asn Arg Val Lys Gly Pro Glu Lys Glu						
115	120	125				
gag aag ttg aga cag gcg gtc aag cag gtg ctg aag tgt gat gtg act	549					
Glu Lys Leu Arg Gln Ala Val Lys Gln Val Leu Lys Cys Asp Val Thr						
130	135	140				
cag agc cag cca ctg ggg gcc gtc ccc tta ccc ccg gct gac tgc gtg	597					
Gln Ser Gln Pro Leu Gly Ala Val Pro Leu Pro Pro Ala Asp Cys Val						

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145	150	155	160	
ctc agc aca ctg tgt ctg gat gcc gcc tgc cca gac ctc ccc acc tac				645
Leu Ser Thr Leu Cys Leu Asp Ala Ala Cys Pro Asp Leu Pro Thr Tyr				
	165	170	175	
tgc agg gcg ctc agg aac ctc ggc agc cta ctg aag cca ggg ggc ttc				693
Cys Arg Ala Leu Arg Asn Leu Gly Ser Leu Leu Lys Pro Gly Gly Phe				
	180	185	190	
ctg gtg atc atg gat gcg ctc aag agc agc tac tac atg att ggt gag				741
Leu Val Ile Met Asp Ala Leu Lys Ser Ser Tyr Tyr Met Ile Gly Glu				
	195	200	205	
cag aag ttc tcc agc ctc ccc ctg ggc cgg gag gca gta gag gct gct				789
Gln Lys Phe Ser Ser Leu Pro Leu Gly Arg Glu Ala Val Glu Ala Ala				
	210	215	220	
gtg aaa gag gct ggc tac aca atc gaa tgg ttt gag gtg atc tcg caa				837
Val Lys Glu Ala Gly Tyr Thr Ile Glu Trp Phe Glu Val Ile Ser Gln				
	225	230	235	240
agt tat tct tcc acc atg gcc aac aac gaa gga ctt ttc tcc ctg gtg				885
Ser Tyr Ser Ser Thr Met Ala Asn Asn Glu Gly Leu Phe Ser Leu Val				
	245	250	255	
gcg agg aag ctg agc aga ccc ctg tgatgcctgt gacctcaatt aaagcaattc				939
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<210> 56

<211> 264

<212> PRT

<213> Homo sapiens

<400> 56

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5

10

15

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50	55	60
Gly Pro Thr Ile Tyr Gln Leu Leu Ser Ala Cys Glu Ser Phe Lys Glu		
65	70	75
Ile Val Val Thr Asp Tyr Ser Asp Gln Asn Leu Gln Glu Leu Glu Lys		
85	90	95
Trp Leu Lys Lys Glu Pro Glu Ala Phe Asp Trp Ser Pro Val Val Thr		
100	105	110
Tyr Val Cys Asp Leu Glu Gly Asn Arg Val Lys Gly Pro Glu Lys Glu		
115	120	125
Glu Lys Leu Arg Gln Ala Val Lys Gln Val Leu Lys Cys Asp Val Thr		
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Gln Ser Gln Pro Leu Gly Ala Val Pro Leu Pro Pro Ala Asp Cys Val		
145	150	155
Leu Ser Thr Leu Cys Leu Asp Ala Ala Cys Pro Asp Leu Pro Thr Tyr		
165	170	175
Cys Arg Ala Leu Arg Asn Leu Gly Ser Leu Leu Lys Pro Gly Gly Phe		
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Leu Val Ile Met Asp Ala Leu Lys Ser Ser Tyr Tyr Met Ile Gly Glu		
195	200	205
Gln Lys Phe Ser Ser Leu Pro Leu Gly Arg Glu Ala Val Glu Ala Ala		
210	215	220
Val Lys Glu Ala Gly Tyr Thr Ile Glu Trp Phe Glu Val Ile Ser Gln		
225	230	235
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<211> 2617

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<213> Homo sapiens

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<222> (94)..(633)

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                               Met Ala Pro Gly Val Ala Arg
                               1           5
ggg ccg acg ccg tac tgg agg ttg cgc ctc ggt ggc gcc gcg ctg ctc 162
Gly Pro Thr Pro Tyr Trp Arg Leu Arg Leu Gly Gly Ala Ala Leu Leu
          10           15           20
ctg ctg ctc atc ccg gtg gcc gcc gcg cag gag cct ccc gga gct gct 210
Leu Leu Leu Ile Pro Val Ala Ala Ala Gln Glu Pro Pro Gly Ala Ala
          25           30           35
tgt tct cag aac aca aac aaa acc tgt gaa gag tgc ctg aag aac gtc 258
Cys Ser Gln Asn Thr Asn Lys Thr Cys Glu Glu Cys Leu Lys Asn Val
          40           45           50           55
tcc tgt ctt tgg tgc aac act aac aag gct tgt ctg gac tac cca gtt 306
Ser Cys Leu Trp Cys Asn Thr Asn Lys Ala Cys Leu Asp Tyr Pro Val
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aca agc gtc ttg cca ccg gct tcc ctt tgt aaa ttg agc tct gca cgc 354
Thr Ser Val Leu Pro Pro Ala Ser Leu Cys Lys Leu Ser Ser Ala Arg
          75           80           85
tgg gga gtt tgt tgg gtg aac ttt gag gcg ctg atc atc acc atg tcg 402
Trp Gly Val Cys Trp Val Asn Phe Glu Ala Leu Ile Ile Thr Met Ser
          90           95          100
gta gtc ggg gga acc ctc ctc ctg ggc att gcc atc tgc tgc tgc tgc 450
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Cys	Cys	Arg	Arg	Lys	Arg	Ser	Arg	Lys	Pro	Asp	Arg	Ser	Glu	Glu	Lys	
120						125					130				135	
gcc	atg	cgt	gag	cgg	gag	gag	agg	cgg	ata	cgg	cag	gag	gaa	cgg	aga	546
Ala	Met	Arg	Glu	Arg	Glu	Glu	Arg	Arg	Ile	Arg	Gln	Glu	Glu	Arg	Arg	
						140					145				150	
gca	gag	atg	aag	aca	aga	cat	gat	gaa	atc	aga	aaa	aaa	tat	ggc	ctg	594
Ala	Glu	Met	Lys	Thr	Arg	His	Asp	Glu	Ile	Arg	Lys	Lys	Tyr	Gly	Leu	
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ttt	aaa	gaa	gaa	aac	ccg	tat	gct	aga	ttt	gaa	aac	aac	taa	agc	gctc	643
Phe	Lys	Glu	Glu	Asn	Pro	Tyr	Ala	Arg	Phe	Glu	Asn	Asn				
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35 40 45
Glu Glu Cys Leu Lys Asn Val Ser Cys Leu Trp Cys Asn Thr Asn Lys
50 55 60
Ala Cys Leu Asp Tyr Pro Val Thr Ser Val Leu Pro Pro Ala Ser Leu
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Cys Lys Leu Ser Ser Ala Arg Trp Gly Val Cys Trp Val Asn Phe Glu

1241.22

85

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95

Ala Leu Ile Ile Thr Met Ser Val Val Gly Gly Thr Leu Leu Leu Gly

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110

Ile Ala Ile Cys Cys Cys Cys Cys Cys Arg Arg Lys Arg Ser Arg Lys

115

120

125

Pro Asp Arg Ser Glu Glu Lys Ala Met Arg Glu Arg Glu Glu Arg Arg

130

135

140

Ile Arg Gln Glu Glu Arg Arg Ala Glu Met Lys Thr Arg His Asp Glu

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175

Phe Glu Asn Asn

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<222> (469)..(1875)

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Met Glu Glu

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Asn Lys Thr Ala Glu Lys Ser Asp Phe Glu Ala Val Glu Ala Leu Met	
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tca atg agc tgc agt tgg aag tct gat ttt aag aaa tac gtt gaa aac	621
Ser Met Ser Cys Ser Trp Lys Ser Asp Phe Lys Lys Tyr Val Glu Asn	
40 45 50	
aga cct gtt aca cca gta tct gat ttg tca gag gaa gag aat ctg ctt	669
Arg Pro Val Thr Pro Val Ser Asp Leu Ser Glu Glu Glu Asn Leu Leu	
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Pro Tyr Ser Pro Ser Asp Phe Glu Pro Ser Gln Val Ser Asn Leu Met	
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Lys Pro His Ile Ala Ala Pro Phe Lys Glu Glu Glu Lys Ser Pro Val	
120 125 130	
tct gcc ccc aaa ctc ccc aaa gct cag gca aca agt gtg att cgt cat	909
Ser Ala Pro Lys Leu Pro Lys Ala Gln Ala Thr Ser Val Ile Arg His	
135 140 145	
aca gct gat gcc cag cta tgt aac cac cag acc tgc cca atg aaa gca	957
Thr Ala Asp Ala Gln Leu Cys Asn His Gln Thr Cys Pro Met Lys Ala	
150 155 160	
gcc agc atc ctc aac tat cag aac aat tct ttt aga aga aga acc cac	1005

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Leu Asn Val Glu Ala Ala Arg Lys Asn Ile Pro Cys Ala Ala Val Ser	
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cca aac aga tcc aaa tgt gag aga aac aca gtg gca gat gtt gat gag	1101
Pro Asn Arg Ser Lys Cys Glu Arg Asn Thr Val Ala Asp Val Asp Glu	
200	205 210
aaa gca agt gct gca ctt tat gac ttt tct gtg cct tcc tca gag acg	1149
Lys Ala Ser Ala Ala Leu Tyr Asp Phe Ser Val Pro Ser Ser Glu Thr	
215	220 225
gtc atc tgc agg tct cag cca gcc cct gtg tcc cca caa cag aag tca	1197
Val Ile Cys Arg Ser Gln Pro Ala Pro Val Ser Pro Gln Gln Lys Ser	
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Val Leu Val Ser Pro Pro Ala Val Ser Ala Gly Gly Val Pro Pro Met	
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Pro Val Ile Cys Gln Met Val Pro Leu Pro Ala Asn Asn Pro Val Val	
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aca aca gtc gtt ccc agc act cct ccc agc cag cca cca gct gtt tgc	1341
Thr Thr Val Val Pro Ser Thr Pro Pro Ser Gln Pro Pro Ala Val Cys	
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Pro Pro Val Val Phe Met Gly Thr Gln Val Pro Lys Gly Ala Val Met	
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Phe Val Val Pro Gln Pro Val Val Gln Ser Ser Lys Pro Pro Val Val	
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agc ccg aat ggc acc aga ctc tct ccc att gcc cct gct cct ggg ttt	1485
Ser Pro Asn Gly Thr Arg Leu Ser Pro Ile Ala Pro Ala Pro Gly Phe	
325	330 335

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Arg Ser His Ile Cys Ser His Pro Gly Cys Gly Lys Thr Tyr Phe Lys
360 365 370
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Ser Ser His Leu Lys Ala His Thr Arg Thr His Thr Gly Glu Lys Pro
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gaa ctg tcc aga cac agg cga acc cac acg ggt gag aag aaa ttt gcg 1725
Glu Leu Ser Arg His Arg Arg Thr His Thr Gly Glu Lys Lys Phe Ala
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Cys Pro Met Cys Asp Arg Arg Phe Met Arg Ser Asp His Leu Thr Lys
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His Ala Arg Arg His Leu Ser Ala Lys Lys Leu Pro Asn Trp Gln Met
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Glu Val Ser Lys Leu Asn Asp Ile Ala Leu Pro Pro Thr Pro Ala Pro
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<212> PRT

<213> Homo sapiens

<400> 60

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Ala Leu Met Ser Met Ser Cys Ser Trp Lys Ser Asp Phe Lys Lys Tyr
          35            40            45
Val Glu Asn Arg Pro Val Thr Pro Val Ser Asp Leu Ser Glu Glu Glu
          50            55            60
Asn Leu Leu Pro Gly Thr Pro Asp Phe His Thr Ile Pro Ala Phe Cys

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Asp Thr Ala Lys Pro His Ile Ala Ala Pro Phe Lys Glu Glu Glu Lys			
115	120	125	
Ser Pro Val Ser Ala Pro Lys Leu Pro Lys Ala Gln Ala Thr Ser Val			
130	135	140	
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Met Lys Ala Ala Ser Ile Leu Asn Tyr Gln Asn Asn Ser Phe Arg Arg			
165	170	175	
Arg Thr His Leu Asn Val Glu Ala Ala Arg Lys Asn Ile Pro Cys Ala			
180	185	190	
Ala Val Ser Pro Asn Arg Ser Lys Cys Glu Arg Asn Thr Val Ala Asp			
195	200	205	
Val Asp Glu Lys Ala Ser Ala Ala Leu Tyr Asp Phe Ser Val Pro Ser			
210	215	220	
Ser Glu Thr Val Ile Cys Arg Ser Gln Pro Ala Pro Val Ser Pro Gln			
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Gln Lys Ser Val Leu Val Ser Pro Pro Ala Val Ser Ala Gly Gly Val			
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Pro Pro Met Pro Val Ile Cys Gln Met Val Pro Leu Pro Ala Asn Asn			
260	265	270	
Pro Val Val Thr Thr Val Val Pro Ser Thr Pro Pro Ser Gln Pro Pro			
275	280	285	
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290	295	300	
Ala Val Met Phe Val Val Pro Gln Pro Val Val Gln Ser Ser Lys Pro			
305	310	315	320
Pro Val Val Ser Pro Asn Gly Thr Arg Leu Ser Pro Ile Ala Pro Ala			

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1241.22

325 330 335
Pro Gly Phe Ser Pro Ser Ala Ala Lys Val Thr Pro Gln Ile Asp Ser
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Ser Arg Ile Arg Ser His Ile Cys Ser His Pro Gly Cys Gly Lys Thr
355 360 365
Tyr Phe Lys Ser Ser His Leu Lys Ala His Thr Arg Thr His Thr Gly
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Glu Lys Pro Phe Ser Cys Ser Trp Lys Gly Cys Glu Arg Arg Phe Ala
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<213> Homo sapiens

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Met Ser Gly Gly Gly Val Ile Arg Gly Pro Ala Gly Asn Asn Asp

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20	25	30		
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Ile Glu Asp Val Phe Tyr Lys Tyr Gly Ala Ile Arg Asp Ile Asp Leu				
35	40	45		
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Lys Asn Arg Arg Gly Gly Pro Pro Phe Ala Phe Val Glu Phe Glu Asp				
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ccg cga gac gcg gaa gac gcg gtg tat ggt cgc gac ggc tat gat tac	361			
Pro Arg Asp Ala Glu Asp Ala Val Tyr Gly Arg Asp Gly Tyr Asp Tyr				
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Tyr Gly Pro Pro Ser Arg Arg Ser Glu Asn Arg Val Val Val Ser Gly				
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ctg cct cca agt gga agt tgg cag gat tta aag gat cac atg cgt gaa	553			
Leu Pro Pro Ser Gly Ser Trp Gln Asp Leu Lys Asp His Met Arg Glu				
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Val Glu Phe Val Arg Lys Glu Asp Met Thr Tyr Ala Val Arg Lys Leu				
160	165	170	175	

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 180 185 190

gtt aaa gtt gat ggg ccc aga agt cca agt tat gga aga tct cga tct 745
 Val Lys Val Asp Gly Pro Arg Ser Pro Ser Tyr Gly Arg Ser Arg Ser
 195 200 205

cga agc cgt agt cgt agc aga agc cgt agc aga agc aac agc agg agt 793
 Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Asn Ser Arg Ser
 210 215 220

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 Arg Ser Tyr Ser Pro Arg Arg Ser Arg Gly Ser Pro Arg Tyr Ser Pro
 225 230 235

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 Arg His Ser Arg Ser Arg Ser Arg Thr
 240 245

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35 40 45

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50 55 60

Arg Asp Ala Glu Asp Ala Val Tyr Gly Arg Asp Gly Tyr Asp Tyr Asp
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Gly Tyr Arg Leu Arg Val Glu Phe Pro Arg Ser Gly Arg Gly Thr Gly
85 90 95

Arg Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Arg Gly Arg Tyr
100 105 110

Gly Pro Pro Ser Arg Arg Ser Glu Asn Arg Val Val Val Ser Gly Leu
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Pro Pro Ser Gly Ser Trp Gln Asp Leu Lys Asp His Met Arg Glu Ala
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145 150 155 160

Glu Phe Val Arg Lys Glu Asp Met Thr Tyr Ala Val Arg Lys Leu Asp
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195 200 205

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<222> (195)..(1943)

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Thr Pro Pro Glu Glu Leu Pro Ser Pro Ser Ala Ser Ser Leu Gly Pro
          30              35              40
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Ile Leu Pro Pro Leu Pro Gly Asp Asp Ser Pro Thr Thr Leu Cys Ser
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Phe Phe Pro Arg Met Ser Asn Leu Arg Leu Ala Asn Pro Ala Gly Gly
          65              70              75
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Arg Pro Gly Ser Lys Gly Glu Pro Gly Arg Ala Ala Asp Asp Gly Glu
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ggg atc gat ggg gca gcc atg cca gag tca ggc ccc cta ccc ctc ctc 518
Gly Ile Asp Gly Ala Ala Met Pro Glu Ser Gly Pro Leu Pro Leu Leu
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gaa ggg ggc cag ctt ggg ggc gag gag tgg acc cgc cac ggg agc ttt	614
Glu Gly Gly Gln Leu Gly Gly Glu Glu Trp Thr Arg His Gly Ser Phe	
125 130 135 140	
gtc aat aag ccc acg cgg ggc tgg ctg cat ccc aac gac aaa gtc atg	662
Val Asn Lys Pro Thr Arg Gly Trp Leu His Pro Asn Asp Lys Val Met	
145 150 155	
gga ccc ggg gtt tcc tac ttg gtt cgg tac atg ggt tgt gtg gag gtc	710
Gly Pro Gly Val Ser Tyr Leu Val Arg Tyr Met Gly Cys Val Glu Val	
160 165 170	
ctc cag tca atg cgt gcc ctg gac ttc aac acc cgg act cag gtc acc	758
Leu Gln Ser Met Arg Ala Leu Asp Phe Asn Thr Arg Thr Gln Val Thr	
175 180 185	
agg gag gcc atc agt ctg gtg tgt gag gct gtg ccg ggt gct aag ggg	806
Arg Glu Ala Ile Ser Leu Val Cys Glu Ala Val Pro Gly Ala Lys Gly	
190 195 200	
gcg aca agg agg aga aag ccc tgt agc cgc ccg ctc agc tct atc ctg	854
Ala Thr Arg Arg Arg Lys Pro Cys Ser Arg Pro Leu Ser Ser Ile Leu	
205 210 215 220	
ggg agg agt aac ctg aaa ttt gct gga atg cca atc act ctc acc gtc	902
Gly Arg Ser Asn Leu Lys Phe Ala Gly Met Pro Ile Thr Leu Thr Val	
225 230 235	
tcc acc agc agc ctc aac ctc atg gcc gca gac tgc aaa cag atc atc	950
Ser Thr Ser Ser Leu Asn Leu Met Ala Ala Asp Cys Lys Gln Ile Ile	
240 245 250	
gcc aac cac cac atg caa tct atc tca ttt gca tcc ggc ggg gat ccg	998
Ala Asn His His Met Gln Ser Ile Ser Phe Ala Ser Gly Gly Asp Pro	
255 260 265	
gac aca gcc gag tat gtc gcc tat gtt gcc aaa gac cct gtg aat cag	1046
Asp Thr Ala Glu Tyr Val Ala Tyr Val Ala Lys Asp Pro Val Asn Gln	

1241.22																		
270						275						280						
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Arg Ala Cys His Ile Leu Glu Cys Pro Glu Gly Leu Ala Gln Asp Val																		
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atc agc acc att ggc cag gcc ttc gag ttg cgc ttc aaa caa tac ctc	1142																	
Ile Ser Thr Ile Gly Gln Ala Phe Glu Leu Arg Phe Lys Gln Tyr Leu																		
					305						310						315	
agg aac cca ccc aaa ctg gtc acc cct cat gac agg atg gct ggc ttt	1190																	
Arg Asn Pro Pro Lys Leu Val Thr Pro His Asp Arg Met Ala Gly Phe																		
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gat ggc tca gca tgg gat gag gag gag gaa gag cca cct gac cat cag	1238																	
Asp Gly Ser Ala Trp Asp Glu Glu Glu Glu Glu Pro Pro Asp His Gln																		
					335						340						345	
tac tat aat gac ttc ccg ggg aag gaa ccc ccc ttg ggg ggg gtg gta	1286																	
Tyr Tyr Asn Asp Phe Pro Gly Lys Glu Pro Pro Leu Gly Gly Val Val																		
					350						355						360	
gac atg agg ctt cgg gaa gga gcc gct cca ggg gct gct cga ccc act	1334																	
Asp Met Arg Leu Arg Glu Gly Ala Ala Pro Gly Ala Ala Arg Pro Thr																		
365						370						375						380
gca ccc aat gcc cag acc ccc agc cac ttg gga gct aca ttg cct gta	1382																	
Ala Pro Asn Ala Gln Thr Pro Ser His Leu Gly Ala Thr Leu Pro Val																		
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gga cag cct gtt ggg gga gat cca gaa gtc cgc aaa cag atg cca cct	1430																	
Gly Gln Pro Val Gly Gly Asp Pro Glu Val Arg Lys Gln Met Pro Pro																		
					400						405						410	
cca cca ccc tgt cca ggc aga gag ctt ttt gat gat ccc tcc tat gtc	1478																	
Pro Pro Pro Cys Pro Gly Arg Glu Leu Phe Asp Asp Pro Ser Tyr Val																		
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aac gtc cag aac cta gac aag gcc cgg caa gca gtg ggt ggt gct ggg	1526																	
Asn Val Gln Asn Leu Asp Lys Ala Arg Gln Ala Val Gly Gly Ala Gly																		
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1241.22

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Pro Pro Asn Pro Ala Ile Asn Gly Ser Ala Pro Arg Asp Leu Phe Asp
445                450                455                460
atg aag ccc ttc gaa gat gct ctt cgg gtg cct cca cct ccc cag tcg 1622
Met Lys Pro Phe Glu Asp Ala Leu Arg Val Pro Pro Pro Pro Gln Ser
                465                470                475
gtg tcc atg gct gag cag ctc cga ggg gag ccc tgg ttc cat ggg aag 1670
Val Ser Met Ala Glu Gln Leu Arg Gly Glu Pro Trp Phe His Gly Lys
                480                485                490
ctg agc cgg cgg gag gct gag gca ctg ctg cag ctc aat ggg gac ttc 1718
Leu Ser Arg Arg Glu Ala Glu Ala Leu Leu Gln Leu Asn Gly Asp Phe
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ttg gta cgg gag agc acg acc aca cct ggc cag tat gtg ctc act ggc 1766
Leu Val Arg Glu Ser Thr Thr Thr Pro Gly Gln Tyr Val Leu Thr Gly
                510                515                520
ttg cag agt ggg cag cct aag cat ttg cta ctg gtg gac cct gag ggt 1814
Leu Gln Ser Gly Gln Pro Lys His Leu Leu Leu Val Asp Pro Glu Gly
525                530                535                540
gtg gtt cgg act aag gat cac cgc ttt gaa agt gtc agt cac ctt atc 1862
Val Val Arg Thr Lys Asp His Arg Phe Glu Ser Val Ser His Leu Ile
                545                550                555
agc tac cac atg gac aat cac ttg ccc atc atc tct gcg ggc agc gaa 1910
Ser Tyr His Met Asp Asn His Leu Pro Ile Ile Ser Ala Gly Ser Glu
                560                565                570
ctg tgt cta cag caa cct gtg gag cgg aaa ctg tgatctgccc tagcgctctc 1963
Leu Cys Leu Gln Gln Pro Val Glu Arg Lys Leu
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atatccagct gagtgagagg gtttgagtca aaagcctggg tgagaatcct gcctctcccc 2143
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ccaacctgat gccccttccc caagaagggtg agtgcttgtc atggaaaatg tcctgtggtg 2263

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1241.22

acaggcccag tggaacagtc acccttctgg gcaaggggga acaaatcaca cctctgggct 2323
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<211> 583

<212> PRT

<213> Homo sapiens

<400> 64

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Glu Leu Pro Ser Pro Ser Ala Ser Ser Leu Gly Pro Ile Leu Pro Pro
35 40 45

Leu Pro Gly Asp Asp Ser Pro Thr Thr Leu Cys Ser Phe Phe Pro Arg
50 55 60

Met Ser Asn Leu Arg Leu Ala Asn Pro Ala Gly Gly Arg Pro Gly Ser
65 70 75 80

Lys Gly Glu Pro Gly Arg Ala Ala Asp Asp Gly Glu Gly Ile Asp Gly
85 90 95

Ala Ala Met Pro Glu Ser Gly Pro Leu Pro Leu Leu Gln Asp Met Asn
100 105 110

Lys Leu Ser Gly Gly Gly Gly Arg Arg Thr Arg Val Glu Gly Gly Gln
115 120 125

Leu Gly Gly Glu Glu Trp Thr Arg His Gly Ser Phe Val Asn Lys Pro
130 135 140

Thr Arg Gly Trp Leu His Pro Asn Asp Lys Val Met Gly Pro Gly Val
145 150 155 160

Ser Tyr Leu Val Arg Tyr Met Gly Cys Val Glu Val Leu Gln Ser Met
165 170 175

Arg Ala Leu Asp Phe Asn Thr Arg Thr Gln Val Thr Arg Glu Ala Ile
180 185 190

Ser Leu Val Cys Glu Ala Val Pro Gly Ala Lys Gly Ala Thr Arg Arg
195 200 205

Arg Lys Pro Cys Ser Arg Pro Leu Ser Ser Ile Leu Gly Arg Ser Asn
210 215 220

Leu Lys Phe Ala Gly Met Pro Ile Thr Leu Thr Val Ser Thr Ser Ser
225 230 235 240

Leu Asn Leu Met Ala Ala Asp Cys Lys Gln Ile Ile Ala Asn His His
245 250 255

Met Gln Ser Ile Ser Phe Ala Ser Gly Gly Asp Pro Asp Thr Ala Glu
260 265 270

1241.22

Tyr Val Ala Tyr Val Ala Lys Asp Pro Val Asn Gln Arg Ala Cys His
275 280 285
Ile Leu Glu Cys Pro Glu Gly Leu Ala Gln Asp Val Ile Ser Thr Ile
290 295 300
Gly Gln Ala Phe Glu Leu Arg Phe Lys Gln Tyr Leu Arg Asn Pro Pro
305 310 315 320
Lys Leu Val Thr Pro His Asp Arg Met Ala Gly Phe Asp Gly Ser Ala
325 330 335
Trp Asp Glu Glu Glu Glu Glu Pro Pro Asp His Gln Tyr Tyr Asn Asp
340 345 350
Phe Pro Gly Lys Glu Pro Pro Leu Gly Gly Val Val Asp Met Arg Leu
355 360 365
Arg Glu Gly Ala Ala Pro Gly Ala Ala Arg Pro Thr Ala Pro Asn Ala
370 375 380
Gln Thr Pro Ser His Leu Gly Ala Thr Leu Pro Val Gly Gln Pro Val
385 390 395 400
Gly Gly Asp Pro Glu Val Arg Lys Gln Met Pro Pro Pro Pro Pro Cys
405 410 415
Pro Gly Arg Glu Leu Phe Asp Asp Pro Ser Tyr Val Asn Val Gln Asn
420 425 430
Leu Asp Lys Ala Arg Gln Ala Val Gly Gly Ala Gly Pro Pro Asn Pro
435 440 445
Ala Ile Asn Gly Ser Ala Pro Arg Asp Leu Phe Asp Met Lys Pro Phe
450 455 460
Glu Asp Ala Leu Arg Val Pro Pro Pro Pro Gln Ser Val Ser Met Ala
465 470 475 480
Glu Gln Leu Arg Gly Glu Pro Trp Phe His Gly Lys Leu Ser Arg Arg
485 490 495
Glu Ala Glu Ala Leu Leu Gln Leu Asn Gly Asp Phe Leu Val Arg Glu
500 505 510
Ser Thr Thr Thr Pro Gly Gln Tyr Val Leu Thr Gly Leu Gln Ser Gly

1241.22

515	520	525	
Gln Pro Lys His Leu Leu Leu Val Asp Pro Glu Gly Val Val Arg Thr			
530	535	540	
Lys Asp His Arg Phe Glu Ser Val Ser His Leu Ile Ser Tyr His Met			
545	550	555	560
Asp Asn His Leu Pro Ile Ile Ser Ala Gly Ser Glu Leu Cys Leu Gln			
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<211> 2493

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (41)..(1237)

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Leu Gly Leu Val Val Cys Leu Val Leu Trp Pro Leu His Ser Glu Gly	
10 15 20	
tct gga ggg aaa ctg aca gct gtg gat cct gaa aca aac atg aat gtg	151
Ser Gly Gly Lys Leu Thr Ala Val Asp Pro Glu Thr Asn Met Asn Val	
25 30 35	
agt gaa att atc tct tac tgg gga ttc cct agt gag gaa tac cta gtt	199
Ser Glu Ile Ile Ser Tyr Trp Gly Phe Pro Ser Glu Glu Tyr Leu Val	
40 45 50	
gag aca gaa gat gga tat att ctg tgc ctt aac cga att cct cat ggg	247
Glu Thr Glu Asp Gly Tyr Ile Leu Cys Leu Asn Arg Ile Pro His Gly	

390

395

tgtaccacca agtcaatgat tatgtcatgt gaaaatgtgt ttgcttcatt tctgtaaaac 1317
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 gatgcccagt tcactctagt ttcaattaga aacatactag ctatTTTTTtC ttttaattagg 1437
 gctggaatag gaagccagtg tctcaaccat agtattgtct ctttaagtct tttaaatattc 1497
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 taaagagctc tctagtctaa cgggtcttga gttagagatc taaatgacat tttatcatgt 1737
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 aacttttcaa taaaattgag tgagacttat aggccc 2493

<210> 66

<211> 399

<212> PRT

<213> Homo sapiens

<400> 66

Met Lys Met Arg Phe Leu Gly Leu Val Val Cys Leu Val Leu Trp Pro

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Leu His Ser Glu Gly Ser Gly Gly Lys Leu Thr Ala Val Asp Pro Glu

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25

30

1241.22

Thr Asn Met Asn Val Ser Glu Ile Ile Ser Tyr Trp Gly Phe Pro Ser
35 40 45
Glu Glu Tyr Leu Val Glu Thr Glu Asp Gly Tyr Ile Leu Cys Leu Asn
50 55 60
Arg Ile Pro His Gly Arg Lys Asn His Ser Asp Lys Gly Pro Lys Pro
65 70 75 80
Val Val Phe Leu Gln His Gly Leu Leu Ala Asp Ser Ser Asn Trp Val
85 90 95
Thr Asn Leu Ala Asn Ser Ser Leu Gly Phe Ile Leu Ala Asp Ala Gly
100 105 110
Phe Asp Val Trp Met Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Lys
115 120 125
His Lys Thr Leu Ser Val Ser Gln Asp Glu Phe Trp Ala Phe Ser Tyr
130 135 140
Asp Glu Met Ala Lys Tyr Asp Leu Pro Ala Ser Ile Asn Phe Ile Leu
145 150 155 160
Asn Lys Thr Gly Gln Glu Gln Val Tyr Tyr Val Gly His Ser Gln Gly
165 170 175
Thr Thr Ile Gly Phe Ile Ala Phe Ser Gln Ile Pro Glu Leu Ala Lys
180 185 190
Arg Ile Lys Met Phe Phe Ala Leu Gly Pro Val Ala Ser Val Ala Phe
195 200 205
Cys Thr Ser Pro Met Ala Lys Leu Gly Arg Leu Pro Asp His Leu Ile
210 215 220
Lys Asp Leu Phe Gly Asp Lys Glu Phe Leu Pro Gln Ser Ala Phe Leu
225 230 235 240
Lys Trp Leu Gly Thr His Val Cys Thr His Val Ile Leu Lys Glu Leu
245 250 255
Cys Gly Asn Leu Cys Phe Leu Leu Cys Gly Phe Asn Glu Arg Asn Leu
260 265 270
Asn Met Ser Arg Val Asp Val Tyr Thr Thr His Ser Pro Ala Gly Thr
275 280 285

1241.22

Ser Val Gln Asn Met Leu His Trp Ser Gln Ala Val Lys Phe Gln Lys
290 295 300
Phe Gln Ala Phe Asp Trp Gly Ser Ser Ala Lys Asn Tyr Phe His Tyr
305 310 315 320
Asn Gln Ser Tyr Pro Pro Thr Tyr Asn Val Lys Asp Met Leu Val Pro
325 330 335
Thr Ala Val Trp Ser Gly Gly His Asp Trp Leu Ala Asp Val Tyr Asp
340 345 350
Val Asn Ile Leu Leu Thr Gln Ile Thr Asn Leu Val Phe His Glu Ser
355 360 365
Ile Pro Glu Trp Glu His Leu Asp Phe Ile Trp Gly Leu Asp Ala Pro
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Trp Arg Leu Tyr Asn Lys Ile Ile Asn Leu Met Arg Lys Tyr Gln
385 390 395

<210> 67

<211> 1633

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (323)..(1177)

<220>

<221>

<222> 1485

<223> unknown

<400> 67

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agcagcagac aggattccag gaaccagtgt ttgatgaagc taggactgag gagcaagcga 180
gcaagcagca gttcgtggaa tcctgtctgc tgctgtcttc ctggtttagg agccgacggg 240
cgctcgcagg ctcagcgcgc gctgcccgcg gcaggacccg gccgcctccg ccgcccgcgc 300

1241.22

cgccccctaag cctcccgaag cc atg gcc ggg ctc ggc cac ccc gcc gcc ttc	352
Met Ala Gly Leu Gly His Pro Ala Ala Phe	
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Gly Arg Ala Thr His Ala Val Val Arg Ala Leu Pro Glu Ser Leu Gly	
15 20 25	
cag cac gcg ctg aga agc gcc aag ggc gag gag gtg gac gtc gcc cgc	448
Gln His Ala Leu Arg Ser Ala Lys Gly Glu Glu Val Asp Val Ala Arg	
30 35 40	
gcg gaa cgg cag cac cag ctc tac gtg ggc gtg ctg ggc agc aag ctg	496
Ala Glu Arg Gln His Gln Leu Tyr Val Gly Val Leu Gly Ser Lys Leu	
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ggg ctg cag gtg gtg gag ctg ccg gcc gac gag agc ctt ccg gac tgc	544
Gly Leu Gln Val Val Glu Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys	
60 65 70	
gtc ttc gtg gag gac gtg gcc gtg gtg tgc gag gag acg gcc ctc atc	592
Val Phe Val Glu Asp Val Ala Val Val Cys Glu Glu Thr Ala Leu Ile	
75 80 85 90	
acc cga ccc ggg gcg ccg agc cgg agg aag gag gtt gac atg atg aaa	640
Thr Arg Pro Gly Ala Pro Ser Arg Arg Lys Glu Val Asp Met Met Lys	
95 100 105	
gaa gca tta gaa aaa ctt cag ctc aat ata gta gag atg aaa gat gaa	688
Glu Ala Leu Glu Lys Leu Gln Leu Asn Ile Val Glu Met Lys Asp Glu	
110 115 120	
aat gca act tta gat ggc gga gat gtt tta ttc aca ggc aga gaa ttt	736
Asn Ala Thr Leu Asp Gly Gly Asp Val Leu Phe Thr Gly Arg Glu Phe	
125 130 135	
ttt gtg ggc ctt tcc aaa agg aca aat caa cga ggt gct gaa atc ttg	784
Phe Val Gly Leu Ser Lys Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu	
140 145 150	
gct gat act ttt aag gac tat gca gtc tcc aca gtg cca gtg gca gat	832

1241.22

Ala Asp Thr Phe Lys Asp Tyr Ala Val Ser Thr Val Pro Val Ala Asp
155 160 165 170
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Gly Leu His Leu Lys Ser Phe Cys Ser Met Ala Gly Pro Asn Leu Ile
175 180 185
gca att ggg tct agt gaa tct gca cag aag gcc ctt aag atc atg caa 928
Ala Ile Gly Ser Ser Glu Ser Ala Gln Lys Ala Leu Lys Ile Met Gln
190 195 200
cag atg agt gac cac cgc tac gac aaa ctc act gtg cct gat gac ata 976
Gln Met Ser Asp His Arg Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile
205 210 215
gca gca aac tgt ata tat cta aat atc ccc aac aaa ggg cac gtc ttg 1024
Ala Ala Asn Cys Ile Tyr Leu Asn Ile Pro Asn Lys Gly His Val Leu
220 225 230
ctg cac cga acc ccg gaa gag tat cca gaa agt gca aag gtt tat gag 1072
Leu His Arg Thr Pro Glu Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu
235 240 245 250
aaa ctg aag gac cat atg ctg atc ccc gtg agc atg tct gaa ctg gaa 1120
Lys Leu Lys Asp His Met Leu Ile Pro Val Ser Met Ser Glu Leu Glu
255 260 265
aag gtg gat ggg ctg ctc acc tgc tgc tca gtt tta att aac aag aaa 1168
Lys Val Asp Gly Leu Leu Thr Cys Cys Ser Val Leu Ile Asn Lys Lys
270 275 280
gta gac tcc tgagctgcag agtccccccc ggtagccggc aagaccgcac 1217
Val Asp Ser
285
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<211> 285

<212> PRT

<213> Homo sapiens

<400> 68

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Ala Lys Gly Glu Glu Val Asp Val Ala Arg Ala Glu Arg Gln His Gln
35 40 45
Leu Tyr Val Gly Val Leu Gly Ser Lys Leu Gly Leu Gln Val Val Glu
50 55 60
Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys Val Phe Val Glu Asp Val
65 70 75 80
Ala Val Val Cys Glu Glu Thr Ala Leu Ile Thr Arg Pro Gly Ala Pro
85 90 95
Ser Arg Arg Lys Glu Val Asp Met Met Lys Glu Ala Leu Glu Lys Leu
100 105 110
Gln Leu Asn Ile Val Glu Met Lys Asp Glu Asn Ala Thr Leu Asp Gly
115 120 125
Gly Asp Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys
130 135 140
Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu Ala Asp Thr Phe Lys Asp
145 150 155 160
Tyr Ala Val Ser Thr Val Pro Val Ala Asp Gly Leu His Leu Lys Ser
165 170 175
Phe Cys Ser Met Ala Gly Pro Asn Leu Ile Ala Ile Gly Ser Ser Glu
180 185 190
Ser Ala Gln Lys Ala Leu Lys Ile Met Gln Gln Met Ser Asp His Arg

1241.22

195	200	205
Tyr Asp Lys Leu Thr Val	Pro Asp Asp Ile Ala Ala	Asn Cys Ile Tyr
210	215	220
Leu Asn Ile Pro Asn Lys Gly His Val	Leu Leu His Arg Thr Pro Glu	
225	230	235
Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu Lys Leu Lys Asp His Met		
245	250	255
Leu Ile Pro Val Ser Met Ser Glu Leu Glu Lys Val Asp Gly Leu Leu		
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Thr Cys Cys Ser Val Leu Ile Asn Lys Lys Val Asp Ser		
275	280	285

<210> 69

<211> 1779

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (147)..(1421)

<400> 69

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gcctcatcta caccctcacc accgcaactt ctcacccgag caagaagcag ctcccagaga 120
gaaagaacgt tcccacctgc ctagcc atg gga gag gac gct gca cag gcc gaa 173

Met Gly Glu Asp Ala Ala Gln Ala Glu

1

5

aag ttc cag cac cct ggg tct gac atg cgg cag gaa aag ccc tcg agc	221
Lys Phe Gln His Pro Gly Ser Asp Met Arg Gln Glu Lys Pro Ser Ser	
10	15
ccc agc ccg atg cct tcc tcc aca cca agc ccc agc ctg aac cta ggg	269
Pro Ser Pro Met Pro Ser Ser Thr Pro Ser Pro Ser Leu Asn Leu Gly	
30	35
aac aca gag gag gcc atc cgg gac aac tca cag gtg aac gca gtc acg	317

1241.22

Asn Thr Glu Glu Ala Ile Arg Asp Asn Ser Gln Val Asn Ala Val Thr	
45 50 55	
gtg ctc acg ctc ctg gac aag ctg gtg aac atg cta gac gct gtg cag	365
Val Leu Thr Leu Leu Asp Lys Leu Val Asn Met Leu Asp Ala Val Gln	
60 65 70	
gag aac cag cac aag atg gag cag cga cag atc agt ttg gag ggc tcc	413
Glu Asn Gln His Lys Met Glu Gln Arg Gln Ile Ser Leu Glu Gly Ser	
75 80 85	
gtg aag ggc atc cag aat gac ctc acc aag ctc tcc aag tac cag gcc	461
Val Lys Gly Ile Gln Asn Asp Leu Thr Lys Leu Ser Lys Tyr Gln Ala	
90 95 100 105	
tcc acc agc aac acg gtg agc aag ctg ctg gag aag tcc cgc aag gtc	509
Ser Thr Ser Asn Thr Val Ser Lys Leu Leu Glu Lys Ser Arg Lys Val	
110 115 120	
agc gcc cac acg cgc gcg gtc aaa gag cgc atg gat agg cag tgc gca	557
Ser Ala His Thr Arg Ala Val Lys Glu Arg Met Asp Arg Gln Cys Ala	
125 130 135	
cag gtg aag cgg ctg gag aac aac cac gcc cag ctc ctc cga cgc aac	605
Gln Val Lys Arg Leu Glu Asn Asn His Ala Gln Leu Leu Arg Arg Asn	
140 145 150	
cat ttc aaa gtg ctc atc ttc cag gag gaa aat gag atc cct gcc agc	653
His Phe Lys Val Leu Ile Phe Gln Glu Glu Asn Glu Ile Pro Ala Ser	
155 160 165	
gtg ttt gtg aaa cag ccc gtt tcc ggt gcc gtg gaa ggg aag gag gag	701
Val Phe Val Lys Gln Pro Val Ser Gly Ala Val Glu Gly Lys Glu Glu	
170 175 180 185	
ctt ccg gat gaa aac aaa tcc ctg gag gaa acc ctg cac acc gtg gac	749
Leu Pro Asp Glu Asn Lys Ser Leu Glu Glu Thr Leu His Thr Val Asp	
190 195 200	
ctc tcc tca gat gat gat ttg ccc cac gat gag gag gcc ctg gaa gac	797
Leu Ser Ser Asp Asp Asp Leu Pro His Asp Glu Glu Ala Leu Glu Asp	

1241.22

205	210	215	
agt gcc gag gaa aag gtg gaa gaa agt agg gca gag aaa ata aaa aga			845
Ser Ala Glu Glu Lys Val Glu Glu Ser Arg Ala Glu Lys Ile Lys Arg			
220	225	230	
tcc agc ctg aag aaa gtg gat agc ctc aag aaa gca ttt tct cgc cag			893
Ser Ser Leu Lys Lys Val Asp Ser Leu Lys Lys Ala Phe Ser Arg Gln			
235	240	245	
aac atc gag aaa aag atg aac aag ctg ggg aca aag atc gta tct gta			941
Asn Ile Glu Lys Lys Met Asn Lys Leu Gly Thr Lys Ile Val Ser Val			
250	255	260	265
gag agg aga gag aag att aag aaa tct ctc acg tca aat cac cag aaa			989
Glu Arg Arg Glu Lys Ile Lys Lys Ser Leu Thr Ser Asn His Gln Lys			
270	275	280	
ata tcc tca gga aaa agc tcc ccc ttc aag gtt tct ccc ctc act ttc			1037
Ile Ser Ser Gly Lys Ser Ser Pro Phe Lys Val Ser Pro Leu Thr Phe			
285	290	295	
ggg cgg aag aaa gtc cga gag gga gaa agc cat gca gaa aat gag acc			1085
Gly Arg Lys Lys Val Arg Glu Gly Glu Ser His Ala Glu Asn Glu Thr			
300	305	310	
aag tca gaa gac ctg cct agc agt gag cag atg cca aat gac cag gaa			1133
Lys Ser Glu Asp Leu Pro Ser Ser Glu Gln Met Pro Asn Asp Gln Glu			
315	320	325	
gag gag tcc ttt gca gag ggt cat tcc gaa gcg tcc ctc gcc agc gct			1181
Glu Glu Ser Phe Ala Glu Gly His Ser Glu Ala Ser Leu Ala Ser Ala			
330	335	340	345
ctg gtg gaa ggg gaa att gca gag gag gct gct gag aag gcg acc tcc			1229
Leu Val Glu Gly Glu Ile Ala Glu Glu Ala Ala Glu Lys Ala Thr Ser			
350	355	360	
agg ggg agt aac tcg ggg atg gac agc aac atc gac ttg act att gtg			1277
Arg Gly Ser Asn Ser Gly Met Asp Ser Asn Ile Asp Leu Thr Ile Val			
365	370	375	
gaa gat gaa gag gag gag tca gtg gcc ctg gaa cag gca cag aag gta			1325

1241.22

Glu Asp Glu Glu Glu Glu Ser Val Ala Leu Glu Gln Ala Gln Lys Val
380 385 390
cgc tat gag ggt agc tac gcg cta aca tcc gag gag gcg gag cgc tcc 1373
Arg Tyr Glu Gly Ser Tyr Ala Leu Thr Ser Glu Glu Ala Glu Arg Ser
395 400 405
gat ggg gac ccc gtg cag ccc gcc gtg ctc cag gtg cac cag acc tcc 1421
Asp Gly Asp Pro Val Gln Pro Ala Val Leu Gln Val His Gln Thr Ser
410 415 420 425
tgagcttaga gccaccgtgc catcctgtgc tgtgctcaag cgggcagcca gggctgaaga 1481
acaaactctt gcacatctcc agcacgactc acccactcct gcgttcctgt ccaggcagta 1541
atcattgacc atatagtcac agtaagacac acgagaccag gctttaccat gaaagcgacc 1601
tgtcacggac tccactttta atttgctctt aggttctatc tctgtagaat gtctccaaga 1661
ttgaagaaga aactgagcag ttgaaaaatg ctaatctctt tgacttagtc agaaaaaac 1721
agaggataat taagatacta gtcataaaaa gtgattcatt cttttttgtc attccatc 1779

<210> 70

<211> 425

<212> PRT

<213> Homo sapiens

<400> 70

Met Gly Glu Asp Ala Ala Gln Ala Glu Lys Phe Gln His Pro Gly Ser
1 5 10 15
Asp Met Arg Gln Glu Lys Pro Ser Ser Pro Ser Pro Met Pro Ser Ser
20 25 30
Thr Pro Ser Pro Ser Leu Asn Leu Gly Asn Thr Glu Glu Ala Ile Arg
35 40 45
Asp Asn Ser Gln Val Asn Ala Val Thr Val Leu Thr Leu Leu Asp Lys
50 55 60
Leu Val Asn Met Leu Asp Ala Val Gln Glu Asn Gln His Lys Met Glu
65 70 75 80
Gln Arg Gln Ile Ser Leu Glu Gly Ser Val Lys Gly Ile Gln Asn Asp

85

90

95

1241.22

Leu Thr Lys Leu Ser Lys Tyr Gln Ala Ser Thr Ser Asn Thr Val Ser			
100	105	110	
Lys Leu Leu Glu Lys Ser Arg Lys Val Ser Ala His Thr Arg Ala Val			
115	120	125	
Lys Glu Arg Met Asp Arg Gln Cys Ala Gln Val Lys Arg Leu Glu Asn			
130	135	140	
Asn His Ala Gln Leu Leu Arg Arg Asn His Phe Lys Val Leu Ile Phe			
145	150	155	160
Gln Glu Glu Asn Glu Ile Pro Ala Ser Val Phe Val Lys Gln Pro Val			
165	170	175	
Ser Gly Ala Val Glu Gly Lys Glu Glu Leu Pro Asp Glu Asn Lys Ser			
180	185	190	
Leu Glu Glu Thr Leu His Thr Val Asp Leu Ser Ser Asp Asp Asp Leu			
195	200	205	
Pro His Asp Glu Glu Ala Leu Glu Asp Ser Ala Glu Glu Lys Val Glu			
210	215	220	
Glu Ser Arg Ala Glu Lys Ile Lys Arg Ser Ser Leu Lys Lys Val Asp			
225	230	235	240
Ser Leu Lys Lys Ala Phe Ser Arg Gln Asn Ile Glu Lys Lys Met Asn			
245	250	255	
Lys Leu Gly Thr Lys Ile Val Ser Val Glu Arg Arg Glu Lys Ile Lys			
260	265	270	
Lys Ser Leu Thr Ser Asn His Gln Lys Ile Ser Ser Gly Lys Ser Ser			
275	280	285	
Pro Phe Lys Val Ser Pro Leu Thr Phe Gly Arg Lys Lys Val Arg Glu			
290	295	300	
Gly Glu Ser His Ala Glu Asn Glu Thr Lys Ser Glu Asp Leu Pro Ser			
305	310	315	320
Ser Glu Gln Met Pro Asn Asp Gln Glu Glu Glu Ser Phe Ala Glu Gly			
325	330	335	
His Ser Glu Ala Ser Leu Ala Ser Ala Leu Val Glu Gly Glu Ile Ala			

1241.22

340	345	350
Glu Glu Ala Ala Glu Lys Ala Thr Ser Arg Gly Ser Asn Ser Gly Met		
355	360	365
Asp Ser Asn Ile Asp Leu Thr Ile Val Glu Asp Glu Glu Glu Glu Ser		
370	375	380
Val Ala Leu Glu Gln Ala Gln Lys Val Arg Tyr Glu Gly Ser Tyr Ala		
385	390	395
400		
Leu Thr Ser Glu Glu Ala Glu Arg Ser Asp Gly Asp Pro Val Gln Pro		
405	410	415
Ala Val Leu Gln Val His Gln Thr Ser		
420	425	

<210> 71

<211> 2638

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (288)..(1844)

<400> 71

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ccagcgtgac ccctgacacg tgtgtgcagc agcctgcagc tgccccaagc catggctgaa 180
cactgactcc cagctgtggg cttcaccatt acagactccc cagggcttca aagacttctc 240
agcttcgagc atggcctttt gctgtcaggg cagctgtaca atagtgg atg ttt gag 296
                                     Met Phe Glu

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1

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acg gag gca gat gag aag agg gag atg gcc ttg gag gaa ggg aag ggg 344
Thr Glu Ala Asp Glu Lys Arg Glu Met Ala Leu Glu Glu Gly Lys Gly
      5              10              15
cct ggt gcc gag gat tcc cca ccc agc aag gag ccc tct cct ggc cag 392
Pro Gly Ala Glu Asp Ser Pro Pro Ser Lys Glu Pro Ser Pro Gly Gln

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1241.22

20	25	30	35	
gag ctt cct cca gga caa gac ctt cca ccc aac aag gac tcc cct tct				440
Glu Leu Pro Pro Gly Gln Asp Leu Pro Pro Asn Lys Asp Ser Pro Ser				
40	45	50		
ggg cag gaa ccc gct ccc agc caa gaa cca ctg tcc agc aaa gac tca				488
Gly Gln Glu Pro Ala Pro Ser Gln Glu Pro Leu Ser Ser Lys Asp Ser				
55	60	65		
gct acc tct gaa gga tcc cct cca ggc cca gat gct ccg ccc agc aag				536
Ala Thr Ser Glu Gly Ser Pro Pro Gly Pro Asp Ala Pro Pro Ser Lys				
70	75	80		
gat gtg cca cca tgc cag gaa ccc cct cca gcc caa gac ctc tca ccc				584
Asp Val Pro Pro Cys Gln Glu Pro Pro Pro Ala Gln Asp Leu Ser Pro				
85	90	95		
tgc cag gac cta cct gct ggt caa gaa ccc ctg cct cac cag gac cct				632
Cys Gln Asp Leu Pro Ala Gly Gln Glu Pro Leu Pro His Gln Asp Pro				
100	105	110	115	
cta ctc acc aaa gac ctc cct gcc atc cag gaa tcc ccc acc cgg gac				680
Leu Leu Thr Lys Asp Leu Pro Ala Ile Gln Glu Ser Pro Thr Arg Asp				
120	125	130		
ctt cca ccc tgt caa gat ctg cct cct agc cag gtc tcc ctg cca gcc				728
Leu Pro Pro Cys Gln Asp Leu Pro Pro Ser Gln Val Ser Leu Pro Ala				
135	140	145		
aag gcc ctt act gag gac acc atg agc tcc ggg gac cta cta gca gct				776
Lys Ala Leu Thr Glu Asp Thr Met Ser Ser Gly Asp Leu Leu Ala Ala				
150	155	160		
act ggg gac cca cct gcg gcc ccc agg cca gcc ttc gtg atc cct gag				824
Thr Gly Asp Pro Pro Ala Ala Pro Arg Pro Ala Phe Val Ile Pro Glu				
165	170	175		
gtc cgg ctg gat agc acc tac agc cag aag gca ggg gca gag cag ggc				872
Val Arg Leu Asp Ser Thr Tyr Ser Gln Lys Ala Gly Ala Glu Gln Gly				
180	185	190	195	
tgc tcg gga gat gag gag gat gca gaa gag gcc gag gag gtg gag gag				920

1241.22

Cys Ser Gly Asp Glu Glu Asp Ala Glu Glu Ala Glu Glu Val Glu Glu	
200 205 210	
ggg gag gaa ggg gag gag gac gag gat gag gac acc agc gat gac aac	968
Gly Glu Glu Gly Glu Glu Asp Glu Asp Glu Asp Thr Ser Asp Asp Asn	
215 220 225	
tac gga gag cgc agt gag gcc aag cgc agc agc atg atc gag acg ggc	1016
Tyr Gly Glu Arg Ser Glu Ala Lys Arg Ser Ser Met Ile Glu Thr Gly	
230 235 240	
cag ggg gct gag ggt ggc ctc tca ctg cgt gtg cag aac tcg ctg cgg	1064
Gln Gly Ala Glu Gly Gly Leu Ser Leu Arg Val Gln Asn Ser Leu Arg	
245 250 255	
cgc cgg acg cac agc gag ggc agc ctg ctg cag gag ccc cga ggg ccc	1112
Arg Arg Thr His Ser Glu Gly Ser Leu Leu Gln Glu Pro Arg Gly Pro	
260 265 270 275	
tgc ttt gcc tcc gac acc acc ttg cac tgc tca gac ggt gag ggc gcc	1160
Cys Phe Ala Ser Asp Thr Thr Leu His Cys Ser Asp Gly Glu Gly Ala	
280 285 290	
gcc tcc acc tgg ggc atg cct tcg ccc agc acc ctc aag aaa gag ctg	1208
Ala Ser Thr Trp Gly Met Pro Ser Pro Ser Thr Leu Lys Lys Glu Leu	
295 300 305	
ggc cgc aat ggt ggc tcc atg cac cac ctt tcc ctc ttc ttc aca gga	1256
Gly Arg Asn Gly Gly Ser Met His His Leu Ser Leu Phe Phe Thr Gly	
310 315 320	
cac agg aag atg agc ggg gct gac acc gtt ggg gat gat gac gaa gcc	1304
His Arg Lys Met Ser Gly Ala Asp Thr Val Gly Asp Asp Asp Glu Ala	
325 330 335	
tcc cgg aag aga aag agc aaa aac cta gcc aag gac atg aag aac aag	1352
Ser Arg Lys Arg Lys Ser Lys Asn Leu Ala Lys Asp Met Lys Asn Lys	
340 345 350 355	
ctg ggg atc ttc aga cgg cgg aat gag tcc cct gga gcc cct ccc gcg	1400
Leu Gly Ile Phe Arg Arg Arg Asn Glu Ser Pro Gly Ala Pro Pro Ala	

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360	365	370	
ggc aag gca gac aaa atg atg aag tca ttc aag ccc acc tca gag gaa			1448
Gly Lys Ala Asp Lys Met Met Lys Ser Phe Lys Pro Thr Ser Glu Glu			
375	380	385	
gcc ctc aag tgg ggc gag tcc ttg gag aag ctg ctg gtt cac aaa tac			1496
Ala Leu Lys Trp Gly Glu Ser Leu Glu Lys Leu Leu Val His Lys Tyr			
390	395	400	
ggg tta gca gtg ttc caa gcc ttc ctt cgc act gag ttc agt gag gag			1544
Gly Leu Ala Val Phe Gln Ala Phe Leu Arg Thr Glu Phe Ser Glu Glu			
405	410	415	
aat ctg gag ttc tgg ttg gct tgt gag gac ttc aag aag gtc aag tca			1592
Asn Leu Glu Phe Trp Leu Ala Cys Glu Asp Phe Lys Lys Val Lys Ser			
420	425	430	435
cag tcc aag atg gca tcc aag gcc aag aag atc ttt gct gaa tac atc			1640
Gln Ser Lys Met Ala Ser Lys Ala Lys Lys Ile Phe Ala Glu Tyr Ile			
440	445	450	
gcg atc cag gca tgc aag gag gtc aac ctg gac tcc tac acg cgg gag			1688
Ala Ile Gln Ala Cys Lys Glu Val Asn Leu Asp Ser Tyr Thr Arg Glu			
455	460	465	
cac acc aag gac aac ctg cag agc gtc acg cgg ggc tgc ttc gac ctg			1736
His Thr Lys Asp Asn Leu Gln Ser Val Thr Arg Gly Cys Phe Asp Leu			
470	475	480	
gca cag aag cgc atc ttc ggg ctc atg gaa aag gac tcg tac cct cgc			1784
Ala Gln Lys Arg Ile Phe Gly Leu Met Glu Lys Asp Ser Tyr Pro Arg			
485	490	495	
ttt ctc cgt tct gac ctc tac ctg gac ctt att aac cag aag aag atg			1832
Phe Leu Arg Ser Asp Leu Tyr Leu Asp Leu Ile Asn Gln Lys Lys Met			
500	505	510	515
agt ccc ccg ctt taggggccac tggagtcgag ctcagcgttc acaccaggcg			1884
Ser Pro Pro Leu			
ggctgggtcc cctgcccacc tgcctccctg cccctgtga cggagggggc aagcaagccc			1944
ccagaggccg tgtctctgga cagacggata gacatacgga agcgaggcct ggaccaagag			2004

1241.22

aggcccaggc tactggagga gtagaaggat gggccccgtg gggccccac tgccccggta 2064
cgagggggcc caagaccctg gcaggtcagg ggcctggcc aagccagatc tggagctgct 2124
gctccctgct gcggagaccg cggaggcttc gcgttgacca agttccttaa agaactggct 2184
gatggggcag gaggtccagg cctgggctct cgggccctcc tagagggcca ttggagcttg 2244
cagctcagac ccccaactttg agttttatatt atttaaata tagttggatg cttggcacgt 2304
cgtcctgtaa taggaaaccc ttgcctcatc agttttcctg atttacaagt gcaatatttt 2364
agccaatgcc ttgggagaag ctgccatgca aaggtggaca ccattctcca gcttcagggg 2424
atatgctcgt cccgggcacc ggtggcaggc agctggcctt ctggactaag gcagcctggg 2484
gggacactgc agtctggcta cacacagaga tctggcacc cctgggtgga gtgtccctcg 2544
ggggctttgg gaaagcatgg caccctcaga ccacacagta gccaagttct ggagcaaata 2604
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<210> 72

<211> 519

<212> PRT

<213> Homo sapiens

<400> 72

Met Phe Glu Thr Glu Ala Asp Glu Lys Arg Glu Met Ala Leu Glu Glu
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Gly Lys Gly Pro Gly Ala Glu Asp Ser Pro Pro Ser Lys Glu Pro Ser
20 25 30
Pro Gly Gln Glu Leu Pro Pro Gly Gln Asp Leu Pro Pro Asn Lys Asp
35 40 45
Ser Pro Ser Gly Gln Glu Pro Ala Pro Ser Gln Glu Pro Leu Ser Ser
50 55 60
Lys Asp Ser Ala Thr Ser Glu Gly Ser Pro Pro Gly Pro Asp Ala Pro
65 70 75 80
Pro Ser Lys Asp Val Pro Pro Cys Gln Glu Pro Pro Pro Ala Gln Asp
85 90 95
Leu Ser Pro Cys Gln Asp Leu Pro Ala Gly Gln Glu Pro Leu Pro His
100 105 110
Gln Asp Pro Leu Leu Thr Lys Asp Leu Pro Ala Ile Gln Glu Ser Pro

1241.22

115	120	125	
Thr Arg Asp Leu Pro Pro Cys Gln Asp Leu Pro Pro Ser Gln Val Ser			
130	135	140	
Leu Pro Ala Lys Ala Leu Thr Glu Asp Thr Met Ser Ser Gly Asp Leu			
145	150	155	160
Leu Ala Ala Thr Gly Asp Pro Pro Ala Ala Pro Arg Pro Ala Phe Val			
165	170	175	
Ile Pro Glu Val Arg Leu Asp Ser Thr Tyr Ser Gln Lys Ala Gly Ala			
180	185	190	
Glu Gln Gly Cys Ser Gly Asp Glu Glu Asp Ala Glu Glu Ala Glu Glu			
195	200	205	
Val Glu Glu Gly Glu Glu Gly Glu Glu Asp Glu Asp Glu Asp Thr Ser			
210	215	220	
Asp Asp Asn Tyr Gly Glu Arg Ser Glu Ala Lys Arg Ser Ser Met Ile			
225	230	235	240
Glu Thr Gly Gln Gly Ala Glu Gly Gly Leu Ser Leu Arg Val Gln Asn			
245	250	255	
Ser Leu Arg Arg Arg Thr His Ser Glu Gly Ser Leu Leu Gln Glu Pro			
260	265	270	
Arg Gly Pro Cys Phe Ala Ser Asp Thr Thr Leu His Cys Ser Asp Gly			
275	280	285	
Glu Gly Ala Ala Ser Thr Trp Gly Met Pro Ser Pro Ser Thr Leu Lys			
290	295	300	
Lys Glu Leu Gly Arg Asn Gly Gly Ser Met His His Leu Ser Leu Phe			
305	310	315	320
Phe Thr Gly His Arg Lys Met Ser Gly Ala Asp Thr Val Gly Asp Asp			
325	330	335	
Asp Glu Ala Ser Arg Lys Arg Lys Ser Lys Asn Leu Ala Lys Asp Met			
340	345	350	
Lys Asn Lys Leu Gly Ile Phe Arg Arg Arg Asn Glu Ser Pro Gly Ala			
355	360	365	

1241.22

Pro Pro Ala Gly Lys Ala Asp Lys Met Met Lys Ser Phe Lys Pro Thr
 370 375 380

Ser Glu Glu Ala Leu Lys Trp Gly Glu Ser Leu Glu Lys Leu Leu Val
 385 390 395 400

His Lys Tyr Gly Leu Ala Val Phe Gln Ala Phe Leu Arg Thr Glu Phe
 405 410 415

Ser Glu Glu Asn Leu Glu Phe Trp Leu Ala Cys Glu Asp Phe Lys Lys
 420 425 430

Val Lys Ser Gln Ser Lys Met Ala Ser Lys Ala Lys Lys Ile Phe Ala
 435 440 445

Glu Tyr Ile Ala Ile Gln Ala Cys Lys Glu Val Asn Leu Asp Ser Tyr
 450 455 460

Thr Arg Glu His Thr Lys Asp Asn Leu Gln Ser Val Thr Arg Gly Cys
 465 470 475 480

Phe Asp Leu Ala Gln Lys Arg Ile Phe Gly Leu Met Glu Lys Asp Ser
 485 490 495

Tyr Pro Arg Phe Leu Arg Ser Asp Leu Tyr Leu Asp Leu Ile Asn Gln
 500 505 510

Lys Lys Met Ser Pro Pro Leu
 515

<210> 73

<211> 1901

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (250)..(1206)

<400> 73

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 gttcccaggt tggaagatta tctcaccg cccagctat ataagctgac cggtgtggag 180

1241.22

gggccagca gggccaactc cagggattcc ttccacgaca gaaaaacata caagactcct 240
tcagccaac atg atg gta ctg aaa gta gag gaa ctg gtc act gga aag aag 291

Met Met Val Leu Lys Val Glu Glu Leu Val Thr Gly Lys Lys

1 5 10

aat ggc aat ggg gag gca ggg gaa ttc ctt cct gag gat ttc aga gat 339
Asn Gly Asn Gly Glu Ala Gly Glu Phe Leu Pro Glu Asp Phe Arg Asp

15 20 25 30

gga gag tat gaa gct gct gtt act tta gag aag cag gag gat ctg aag 387
Gly Glu Tyr Glu Ala Ala Val Thr Leu Glu Lys Gln Glu Asp Leu Lys

35 40 45

aca ctt cta gcc cac cct gtg acc ctg ggg gag caa cag tgg aaa agc 435
Thr Leu Leu Ala His Pro Val Thr Leu Gly Glu Gln Gln Trp Lys Ser

50 55 60

gag aaa caa cga gag gca gag ctc cca aag aaa aaa cta gaa caa aga 483
Glu Lys Gln Arg Glu Ala Glu Leu Pro Lys Lys Lys Leu Glu Gln Arg

65 70 75

tcc aag ctt gaa aat tta gaa gac ctt gaa ata atc att caa ctg aag 531
Ser Lys Leu Glu Asn Leu Glu Asp Leu Glu Ile Ile Ile Gln Leu Lys

80 85 90

aaa agg aaa aaa tac agg aaa act aaa gtt cca gtt gta aag gaa cca 579
Lys Arg Lys Lys Tyr Arg Lys Thr Lys Val Pro Val Val Lys Glu Pro

95 100 105 110

gaa cct gaa atc att acg gaa cct gtg gat gtg cct acg ttt ctg aag 627
Glu Pro Glu Ile Ile Thr Glu Pro Val Asp Val Pro Thr Phe Leu Lys

115 120 125

gct gct ctg gag aat aaa ctg cca gta gta gaa aaa ttc ttg tca gac 675
Ala Ala Leu Glu Asn Lys Leu Pro Val Val Glu Lys Phe Leu Ser Asp

130 135 140

aag aac aat cca gat gtt tgt gat gag tat aaa cgg aca gct ctt cat 723
Lys Asn Asn Pro Asp Val Cys Asp Glu Tyr Lys Arg Thr Ala Leu His

145 150 155

aga gca tgc ttg gaa gga cat ttg gca att gtg gag aag tta atg gaa 771

1241.22

Arg Ala Cys Leu Glu Gly His Leu Ala Ile Val Glu Lys Leu Met Glu	
160 165 170	
gct gga gcc cag atc gaa ttc cgt gat atg ctt gaa tcc aca gcc atc	819
Ala Gly Ala Gln Ile Glu Phe Arg Asp Met Leu Glu Ser Thr Ala Ile	
175 180 185 190	
cac tgg gca agc cgt gga gga aac ctg gat gtt tta aaa ttg ttg ctg	867
His Trp Ala Ser Arg Gly Gly Asn Leu Asp Val Leu Lys Leu Leu Leu	
195 200 205	
aat aaa gga gca aaa att agc gcc cga gat aag ttg ctc agc aca gcg	915
Asn Lys Gly Ala Lys Ile Ser Ala Arg Asp Lys Leu Leu Ser Thr Ala	
210 215 220	
ctg cat gtg gcg gtg agg act ggc cac tat gag tgc gcg gag cat ctt	963
Leu His Val Ala Val Arg Thr Gly His Tyr Glu Cys Ala Glu His Leu	
225 230 235	
atc gcc tgt gag gca gac ctc aac gcc aaa gac aga gaa gga gat acc	1011
Ile Ala Cys Glu Ala Asp Leu Asn Ala Lys Asp Arg Glu Gly Asp Thr	
240 245 250	
ccg ttg cat gat gcg gtg aga ctg aac cgc tat aag atg atc cga ctc	1059
Pro Leu His Asp Ala Val Arg Leu Asn Arg Tyr Lys Met Ile Arg Leu	
255 260 265 270	
ctg att atg tat ggc gcg gat ctc aac atc aag aac tgt gct ggg aag	1107
Leu Ile Met Tyr Gly Ala Asp Leu Asn Ile Lys Asn Cys Ala Gly Lys	
275 280 285	
acg ccg atg gat ctg gtg cta cac tgg cag aat gga acc aaa gca ata	1155
Thr Pro Met Asp Leu Val Leu His Trp Gln Asn Gly Thr Lys Ala Ile	
290 295 300	
ttc gac agc ctc aga gag aac tcc tac aag acc tct cgc ata gct aca	1203
Phe Asp Ser Leu Arg Glu Asn Ser Tyr Lys Thr Ser Arg Ile Ala Thr	
305 310 315	
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Phe	

1241.22

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<211> 319

<212> PRT

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<400> 74

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			20					25						30	
Tyr	Glu	Ala	Ala	Val	Thr	Leu	Glu	Lys	Gln	Glu	Asp	Leu	Lys	Thr	Leu
			35					40						45	
Leu	Ala	His	Pro	Val	Thr	Leu	Gly	Glu	Gln	Gln	Trp	Lys	Ser	Glu	Lys
			50					55						60	
Gln	Arg	Glu	Ala	Glu	Leu	Pro	Lys	Lys	Lys	Leu	Glu	Gln	Arg	Ser	Lys
			65					70						75	
Leu	Glu	Asn	Leu	Glu	Asp	Leu	Glu	Ile	Ile	Ile	Gln	Leu	Lys	Lys	Arg
								85						90	
Lys	Lys	Tyr	Arg	Lys	Thr	Lys	Val	Pro	Val	Val	Lys	Glu	Pro	Glu	Pro
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Glu	Ile	Ile	Thr	Glu	Pro	Val	Asp	Val	Pro	Thr	Phe	Leu	Lys	Ala	Ala

1241.22

115	120	125
Leu Glu Asn Lys Leu Pro Val Val Glu Lys Phe Leu Ser Asp Lys Asn		
130	135	140
Asn Pro Asp Val Cys Asp Glu Tyr Lys Arg Thr Ala Leu His Arg Ala		
145	150	155
Cys Leu Glu Gly His Leu Ala Ile Val Glu Lys Leu Met Glu Ala Gly		
165	170	175
Ala Gln Ile Glu Phe Arg Asp Met Leu Glu Ser Thr Ala Ile His Trp		
180	185	190
Ala Ser Arg Gly Gly Asn Leu Asp Val Leu Lys Leu Leu Leu Asn Lys		
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Gly Ala Lys Ile Ser Ala Arg Asp Lys Leu Leu Ser Thr Ala Leu His		
210	215	220
Val Ala Val Arg Thr Gly His Tyr Glu Cys Ala Glu His Leu Ile Ala		
225	230	235
Cys Glu Ala Asp Leu Asn Ala Lys Asp Arg Glu Gly Asp Thr Pro Leu		
245	250	255
His Asp Ala Val Arg Leu Asn Arg Tyr Lys Met Ile Arg Leu Leu Ile		
260	265	270
Met Tyr Gly Ala Asp Leu Asn Ile Lys Asn Cys Ala Gly Lys Thr Pro		
275	280	285
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<210> 75

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<213> Homo sapiens

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<222> (118)..(5475)

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atg ggg ctt ctc cag ttg cta gct ttc agt ttc tta gcc ctg tgc aga 165
Met Gly Leu Leu Gln Leu Leu Ala Phe Ser Phe Leu Ala Leu Cys Arg
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gcc cga gtg cgc gct cag gaa ccc gag ttc agc tac ggc tgc gca gaa 213
Ala Arg Val Arg Ala Gln Glu Pro Glu Phe Ser Tyr Gly Cys Ala Glu
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Gly Ser Cys Tyr Pro Ala Thr Gly Asp Leu Leu Ile Gly Arg Ala Gln
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Lys Leu Ser Val Thr Ser Thr Cys Gly Leu His Lys Pro Glu Pro Tyr
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Cys Ile Val Ser His Leu Gln Glu Asp Lys Lys Cys Phe Ile Cys Asn
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Ser Gln Asp Pro Tyr His Glu Thr Leu Asn Pro Asp Ser His Leu Ile
          85          90          95
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Glu Asn Val Val Thr Thr Phe Ala Pro Asn Arg Leu Lys Ile Trp Trp
          100          105          110
caa tct gaa aat ggt gtg gaa aat gta act atc caa ctg gat ttg gaa 501
Gln Ser Glu Asn Gly Val Glu Asn Val Thr Ile Gln Leu Asp Leu Glu
          115          120          125
gca gaa ttc cat ttt act cat ctc ata atg act ttc aag aca ttc cgt 549
Ala Glu Phe His Phe Thr His Leu Ile Met Thr Phe Lys Thr Phe Arg
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Gly	Val	Tyr	Arg	Tyr	Phe	Ala	Tyr	Asp	Cys	Glu	Ala	Ser	Phe	Pro	Gly	
				165					170					175		
att	tca	act	ggc	ccc	atg	aaa	aaa	gtc	gat	gac	ata	att	tgt	gat	tct	693
Ile	Ser	Thr	Gly	Pro	Met	Lys	Lys	Val	Asp	Asp	Ile	Ile	Cys	Asp	Ser	
			180					185					190			
cga	tat	tct	gac	att	gaa	ccc	tca	act	gaa	gga	gag	gtg	ata	ttt	cgt	741
Arg	Tyr	Ser	Asp	Ile	Glu	Pro	Ser	Thr	Glu	Gly	Glu	Val	Ile	Phe	Arg	
		195					200					205				
gct	tta	gat	cct	gct	ttc	aaa	ata	gaa	gat	cct	tat	agc	cca	agg	ata	789
Ala	Leu	Asp	Pro	Ala	Phe	Lys	Ile	Glu	Asp	Pro	Tyr	Ser	Pro	Arg	Ile	
	210					215					220					
cag	aat	tta	tta	aaa	att	acc	aac	ttg	aga	atc	aag	ttt	gtg	aaa	ctg	837
Gln	Asn	Leu	Leu	Lys	Ile	Thr	Asn	Leu	Arg	Ile	Lys	Phe	Val	Lys	Leu	
225				230					235					240		
cat	act	ttg	gga	gat	aac	ctt	ctg	gat	tcc	agg	atg	gaa	atc	aga	gaa	885
His	Thr	Leu	Gly	Asp	Asn	Leu	Leu	Asp	Ser	Arg	Met	Glu	Ile	Arg	Glu	
			245						250				255			
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Lys	Tyr	Tyr	Tyr	Ala	Val	Tyr	Asp	Met	Val	Val	Arg	Gly	Asn	Cys	Phe	
			260					265				270				
tgc	tat	ggt	cat	gcc	agc	gaa	tgt	gcc	cct	gtg	gat	gga	ttc	aat	gaa	981
Cys	Tyr	Gly	His	Ala	Ser	Glu	Cys	Ala	Pro	Val	Asp	Gly	Phe	Asn	Glu	
		275					280					285				
gaa	gtg	gaa	gga	atg	gtt	cac	gga	cac	tgc	atg	tgc	agg	cat	aac	acc	1029
Glu	Val	Glu	Gly	Met	Val	His	Gly	His	Cys	Met	Cys	Arg	His	Asn	Thr	
	290					295					300					
aag	ggc	tta	aac	tgt	gaa	ctc	tgc	atg	gat	ttc	tac	cat	gat	tta	cct	1077
Lys	Gly	Leu	Asn	Cys	Glu	Leu	Cys	Met	Asp	Phe	Tyr	His	Asp	Leu	Pro	

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Trp Arg Pro Ala Glu Gly Arg Asn Ser Asn Ala Cys Lys Lys Cys Asn			
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tgc aat gaa cat tcc atc tct tgt cac ttt gac atg gct gtt tac ctg			1173
Cys Asn Glu His Ser Ile Ser Cys His Phe Asp Met Ala Val Tyr Leu			
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gcc acg ggg aac gtc agc gga ggc gtg tgt gat gac tgt cag cac aac			1221
Ala Thr Gly Asn Val Ser Gly Gly Val Cys Asp Asp Cys Gln His Asn			
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acc atg ggg cgc aac tgt gag cag tgc aag ccg ttt tac tac cag cac			1269
Thr Met Gly Arg Asn Cys Glu Gln Cys Lys Pro Phe Tyr Tyr Gln His			
	370	375	380
cca gag agg gac atc cga gat cct aat ttc tgt gaa cga tgt acg tgt			1317
Pro Glu Arg Asp Ile Arg Asp Pro Asn Phe Cys Glu Arg Cys Thr Cys			
385	390	395	400
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Asp Pro Ala Gly Ser Gln Asn Glu Gly Ile Cys Asp Ser Tyr Thr Asp			
	405	410	415
ttt tct act ggt ctc att gct ggc cag tgt cgg tgt aaa tta aat gtg			1413
Phe Ser Thr Gly Leu Ile Ala Gly Gln Cys Arg Cys Lys Leu Asn Val			
	420	425	430
gaa gga gaa cat tgt gat gtt tgc aaa gaa ggc ttc tat gat tta agc			1461
Glu Gly Glu His Cys Asp Val Cys Lys Glu Gly Phe Tyr Asp Leu Ser			
	435	440	445
agt gaa gat cca ttt ggt tgt aaa tct tgt gct tgc aat cct ctg gga			1509
Ser Glu Asp Pro Phe Gly Cys Lys Ser Cys Ala Cys Asn Pro Leu Gly			
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aca att cct gga ggg aat cct tgt gat tcc gag aca ggt cac tgc tac			1557
Thr Ile Pro Gly Gly Asn Pro Cys Asp Ser Glu Thr Gly His Cys Tyr			
465	470	475	480
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His Trp Gly Leu Ser Asn Asp Leu Asp Gly Cys Arg Pro Cys Asp Cys	
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gac ctt ggg gga gcc tta aac aac agt tgc ttt gcg gag tca ggc cag	1701
Asp Leu Gly Gly Ala Leu Asn Asn Ser Cys Phe Ala Glu Ser Gly Gln	
515 520 525	
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Cys Ser Cys Arg Pro His Met Ile Gly Arg Gln Cys Asn Glu Val Glu	
530 535 540	
cct ggt tac tac ttt gcc acc ctg gat cac tac ctc tat gaa gcg gag	1797
Pro Gly Tyr Tyr Phe Ala Thr Leu Asp His Tyr Leu Tyr Glu Ala Glu	
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Glu Ala Asn Leu Gly Pro Gly Val Ser Ile Val Glu Arg Gln Tyr Ile	
565 570 575	
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Gln Asp Arg Ile Pro Ser Trp Thr Gly Ala Gly Phe Val Arg Val Pro	
580 585 590	
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Glu Gly Ala Tyr Leu Glu Phe Phe Ile Asp Asn Ile Pro Tyr Ser Met	
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Glu Tyr Asp Ile Leu Ile Arg Tyr Glu Pro Gln Leu Pro Asp His Trp	
610 615 620	
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Glu Lys Ala Val Ile Thr Val Gln Arg Pro Gly Arg Ile Pro Thr Ser	
625 630 635 640	
agc cga tgt ggt aat acc atc ccc gat gat gac aac cag gtg gtg tca	2085
Ser Arg Cys Gly Asn Thr Ile Pro Asp Asp Asp Asn Gln Val Val Ser	

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gag aag gga aca aac tac acg gtg agg ttg gag ctg cct cag tac acc			2181
Glu Lys Gly Thr Asn Tyr Thr Val Arg Leu Glu Leu Pro Gln Tyr Thr			
675	680	685	
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Ser Ser Asp Ser Asp Val Glu Ser Pro Tyr Thr Leu Ile Asp Ser Leu			
690	695	700	
gtt ctc atg cca tac tgt aaa tca ctg gac atc ttc acc gtg gga ggt			2277
Val Leu Met Pro Tyr Cys Lys Ser Leu Asp Ile Phe Thr Val Gly Gly			
705	710	715	720
tca gga gat ggg gtg gtc acc aac agt gcc tgg gaa acc ttt cag aga			2325
Ser Gly Asp Gly Val Val Thr Asn Ser Ala Trp Glu Thr Phe Gln Arg			
725	730	735	
tac cga tgt cta gag aac agc aga agc gtt gtg aaa aca ccg atg aca			2373
Tyr Arg Cys Leu Glu Asn Ser Arg Ser Val Val Lys Thr Pro Met Thr			
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Asp Val Cys Arg Asn Ile Ile Phe Ser Ile Ser Ala Leu Leu His Gln			
755	760	765	
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Thr Gly Leu Ala Cys Glu Cys Asp Pro Gln Gly Ser Leu Ser Ser Val			
770	775	780	
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Cys Asp Pro Asn Gly Gly Gln Cys Gln Cys Arg Pro Asn Val Val Gly			
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aga acc tgc aac aga tgt gca cct gga act ttt ggc ttt ggc ccc agt			2565
Arg Thr Cys Asn Arg Cys Ala Pro Gly Thr Phe Gly Phe Gly Pro Ser			
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Gln Pro Cys Gln Cys Asn Gly His Ala Asp Asp Cys Asp Pro Val Thr	
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Gly Glu Cys Leu Asn Cys Gln Asp Tyr Thr Met Gly His Asn Cys Glu	
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Arg Cys Leu Ala Gly Tyr Tyr Gly Asp Pro Ile Ile Gly Ser Gly Asp	
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His Cys Arg Pro Cys Pro Cys Pro Asp Gly Pro Asp Ser Gly Arg Gln	
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Phe Ala Arg Ser Cys Tyr Gln Asp Pro Val Thr Leu Gln Leu Ala Cys	
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Val Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys Asp Asp Cys Ala Ser	
945 950 955 960	
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Gly Tyr Phe Gly Asn Pro Ser Glu Val Gly Gly Ser Cys Gln Pro Cys	
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Gln Cys His Asn Asn Ile Asp Thr Thr Asp Pro Glu Ala Cys Asp Lys	

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980	985	990	
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Cys Gln Phe Cys Arg Phe Gly Tyr Tyr Gly Asp Ala Leu Arg Gln Asp			
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Cys Arg Lys Cys Val Cys Asn Tyr Leu Gly Thr Val Gln Glu His Cys			
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Leu Pro Asn Val Ile Gly Gln Asn Cys Asp Arg Cys Ala Pro Asn Thr			
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Trp Gln Leu Ala Ser Gly Thr Gly Cys Asp Pro Cys Asn Cys Asn Ala			
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Phe Trp Gly Asp Pro Asp Val Glu Cys Arg Ala Cys Asp Cys Asp Pro			
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Leu Trp Asp Val Ile Ile Ala Glu Leu Thr Asn Arg Thr His Arg Phe	
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Thr Ala Lys Glu Leu Asp Ser Leu Gln Thr Glu Ala Glu Ser Leu Asp	
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Asp Ile Arg Gly Ala Leu Asp Ser Ile Thr Lys Tyr Phe Gln Met Ser	

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atg gag cga gaa tcc cag ttc aag gaa aaa caa gag gag cag gct cgc			4245
Met Glu Arg Glu Ser Gln Phe Lys Glu Lys Gln Glu Glu Gln Ala Arg			
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Leu Leu Asp Glu Leu Ala Gly Lys Leu Gln Ser Leu Asp Leu Ser Ala			
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Ala Ala Glu Met Thr Cys Gly Thr Pro Pro Gly Ala Ser Cys Ser Glu			
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Thr Glu Cys Gly Gly Pro Asn Cys Arg Thr Asp Glu Gly Glu Arg Lys			
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Cys Gly Gly Pro Gly Cys Gly Gly Leu Val Thr Val Ala His Asn Ala			
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Glu Val Glu Gln Leu Ser Lys Met Val Ser Glu Ala Lys Leu Arg Ala			
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Asp Glu Ala Lys Gln Ser Ala Glu Asp Ile Leu Leu Lys Thr Asn Ala			
1475	1480	1485	
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Thr Lys Glu Lys Met Asp Lys Ser Asn Glu Glu Leu Arg Asn Leu Ile	
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Lys Gln Ile Arg Asn Phe Leu Thr Gln Asp Ser Ala Asp Leu Asp Ser	
1505	1510 1515 1520
att gaa gca gtt gct aat gaa gta ttg aaa atg gag atg cct agc acc	4725
Ile Glu Ala Val Ala Asn Glu Val Leu Lys Met Glu Met Pro Ser Thr	
1525	1530 1535
cca cag cag tta cag aac ttg aca gaa gat ata cgt gaa cga gtt gaa	4773
Pro Gln Gln Leu Gln Asn Leu Thr Glu Asp Ile Arg Glu Arg Val Glu	
1540	1545 1550
agc ctt tct caa gta gag gtt att ctt cag cat agt gct gct gac att	4821
Ser Leu Ser Gln Val Glu Val Ile Leu Gln His Ser Ala Ala Asp Ile	
1555	1560 1565
gcc aga gct gag atg ttg tta gaa gaa gct aaa aga gca agc aaa agt	4869
Ala Arg Ala Glu Met Leu Leu Glu Glu Ala Lys Arg Ala Ser Lys Ser	
1570	1575 1580
gca aca gat gtt aaa gtc act gca gat atg gta aag gaa gct ctg gaa	4917
Ala Thr Asp Val Lys Val Thr Ala Asp Met Val Lys Glu Ala Leu Glu	
1585	1590 1595 1600
gaa gca gaa aag gcc cag gtc gca gca gag aag gca att aaa caa gca	4965
Glu Ala Glu Lys Ala Gln Val Ala Ala Glu Lys Ala Ile Lys Gln Ala	
1605	1610 1615
gat gaa gac att caa gga acc cag aac ctg tta act tcg att gag tct	5013
Asp Glu Asp Ile Gln Gly Thr Gln Asn Leu Leu Thr Ser Ile Glu Ser	
1620	1625 1630
gaa aca gca gct tct gag gaa acc ttg ttc aac gcg tcc cag cgc atc	5061
Glu Thr Ala Ala Ser Glu Glu Thr Leu Phe Asn Ala Ser Gln Arg Ile	
1635	1640 1645
agc gag tta gag agg aat gtg gaa gaa ctt aag cgg aaa gct gcc caa	5109
Ser Glu Leu Glu Arg Asn Val Glu Glu Leu Lys Arg Lys Ala Ala Gln	

		1241.22	
1650	1655	1660	
aac tcc ggg gag gca gaa tat att gaa aaa gta gta tat act gtg aag			5157
Asn Ser Gly Glu Ala Glu Tyr Ile Glu Lys Val Val Tyr Thr Val Lys			
1665	1670	1675	1680
caa agt gca gaa gat gtt aag aag act tta gat ggt gaa ctt gat gaa			5205
Gln Ser Ala Glu Asp Val Lys Lys Thr Leu Asp Gly Glu Leu Asp Glu			
	1685	1690	1695
aag tat aaa aaa gta gaa aat tta att gcc aaa aaa act gaa gag tca			5253
Lys Tyr Lys Lys Val Glu Asn Leu Ile Ala Lys Lys Thr Glu Glu Ser			
	1700	1705	1710
gct gat gcc aga agg aaa gcc gaa atg cta caa aat gaa gca aaa act			5301
Ala Asp Ala Arg Arg Lys Ala Glu Met Leu Gln Asn Glu Ala Lys Thr			
	1715	1720	1725
ctt tta gct caa gca aat agc aag ctg caa ctg ctc aaa gat tta gaa			5349
Leu Leu Ala Gln Ala Asn Ser Lys Leu Gln Leu Leu Lys Asp Leu Glu			
	1730	1735	1740
aga aaa tat gaa gac aat caa aga tac tta gaa gat aaa gct caa gaa			5397
Arg Lys Tyr Glu Asp Asn Gln Arg Tyr Leu Glu Asp Lys Ala Gln Glu			
1745	1750	1755	1760
tta gca aga ctg gaa gga gaa gtc cgt tca ctc cta aag gat ata agc			5445
Leu Ala Arg Leu Glu Gly Glu Val Arg Ser Leu Leu Lys Asp Ile Ser			
	1765	1770	1775
cag aaa gtt gct gtg tat agc aca tgc ttg taacagagga gaataaaaaa			5495
Gln Lys Val Ala Val Tyr Ser Thr Cys Leu			
	1780	1785	
tggtgaggt gaacaaggta aaacaactac attttaaaaa ctgacttaat gctcttcaaa			5555
ataaaacatc acctatttaa tgtttttaac cacattttgt atgagttaaa taaagccc			5613

<210> 76

<211> 1786

<212> PRT

<213> Homo sapiens

1241.22

<400> 76

Met Gly Leu Leu Gln Leu Leu Ala Phe Ser Phe Leu Ala Leu Cys Arg
1 5 10 15
Ala Arg Val Arg Ala Gln Glu Pro Glu Phe Ser Tyr Gly Cys Ala Glu
20 25 30
Gly Ser Cys Tyr Pro Ala Thr Gly Asp Leu Leu Ile Gly Arg Ala Gln
35 40 45
Lys Leu Ser Val Thr Ser Thr Cys Gly Leu His Lys Pro Glu Pro Tyr
50 55 60
Cys Ile Val Ser His Leu Gln Glu Asp Lys Lys Cys Phe Ile Cys Asn
65 70 75 80
Ser Gln Asp Pro Tyr His Glu Thr Leu Asn Pro Asp Ser His Leu Ile
85 90 95
Glu Asn Val Val Thr Thr Phe Ala Pro Asn Arg Leu Lys Ile Trp Trp
100 105 110
Gln Ser Glu Asn Gly Val Glu Asn Val Thr Ile Gln Leu Asp Leu Glu
115 120 125
Ala Glu Phe His Phe Thr His Leu Ile Met Thr Phe Lys Thr Phe Arg
130 135 140
Pro Ala Ala Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp
145 150 155 160
Gly Val Tyr Arg Tyr Phe Ala Tyr Asp Cys Glu Ala Ser Phe Pro Gly
165 170 175
Ile Ser Thr Gly Pro Met Lys Lys Val Asp Asp Ile Ile Cys Asp Ser
180 185 190
Arg Tyr Ser Asp Ile Glu Pro Ser Thr Glu Gly Glu Val Ile Phe Arg
195 200 205
Ala Leu Asp Pro Ala Phe Lys Ile Glu Asp Pro Tyr Ser Pro Arg Ile
210 215 220
Gln Asn Leu Leu Lys Ile Thr Asn Leu Arg Ile Lys Phe Val Lys Leu
225 230 235 240
His Thr Leu Gly Asp Asn Leu Leu Asp Ser Arg Met Glu Ile Arg Glu

1241.22

245	250	255
Lys Tyr Tyr Tyr Ala Val Tyr Asp Met Val Val Arg Gly Asn Cys Phe		
260	265	270
Cys Tyr Gly His Ala Ser Glu Cys Ala Pro Val Asp Gly Phe Asn Glu		
275	280	285
Glu Val Glu Gly Met Val His Gly His Cys Met Cys Arg His Asn Thr		
290	295	300
Lys Gly Leu Asn Cys Glu Leu Cys Met Asp Phe Tyr His Asp Leu Pro		
305	310	315
Trp Arg Pro Ala Glu Gly Arg Asn Ser Asn Ala Cys Lys Lys Cys Asn		
325	330	335
Cys Asn Glu His Ser Ile Ser Cys His Phe Asp Met Ala Val Tyr Leu		
340	345	350
Ala Thr Gly Asn Val Ser Gly Gly Val Cys Asp Asp Cys Gln His Asn		
355	360	365
Thr Met Gly Arg Asn Cys Glu Gln Cys Lys Pro Phe Tyr Tyr Gln His		
370	375	380
Pro Glu Arg Asp Ile Arg Asp Pro Asn Phe Cys Glu Arg Cys Thr Cys		
385	390	395
Asp Pro Ala Gly Ser Gln Asn Glu Gly Ile Cys Asp Ser Tyr Thr Asp		
405	410	415
Phe Ser Thr Gly Leu Ile Ala Gly Gln Cys Arg Cys Lys Leu Asn Val		
420	425	430
Glu Gly Glu His Cys Asp Val Cys Lys Glu Gly Phe Tyr Asp Leu Ser		
435	440	445
Ser Glu Asp Pro Phe Gly Cys Lys Ser Cys Ala Cys Asn Pro Leu Gly		
450	455	460
Thr Ile Pro Gly Gly Asn Pro Cys Asp Ser Glu Thr Gly His Cys Tyr		
465	470	475
Cys Lys Arg Leu Val Thr Gly Gln His Cys Asp Gln Cys Leu Pro Glu		
485	490	495

1241.22

His Trp Gly Leu Ser Asn Asp Leu Asp Gly Cys Arg Pro Cys Asp Cys
500 505 510

Asp Leu Gly Gly Ala Leu Asn Asn Ser Cys Phe Ala Glu Ser Gly Gln
515 520 525

Cys Ser Cys Arg Pro His Met Ile Gly Arg Gln Cys Asn Glu Val Glu
530 535 540

Pro Gly Tyr Tyr Phe Ala Thr Leu Asp His Tyr Leu Tyr Glu Ala Glu
545 550 555 560

Glu Ala Asn Leu Gly Pro Gly Val Ser Ile Val Glu Arg Gln Tyr Ile
565 570 575

Gln Asp Arg Ile Pro Ser Trp Thr Gly Ala Gly Phe Val Arg Val Pro
580 585 590

Glu Gly Ala Tyr Leu Glu Phe Phe Ile Asp Asn Ile Pro Tyr Ser Met
595 600 605

Glu Tyr Asp Ile Leu Ile Arg Tyr Glu Pro Gln Leu Pro Asp His Trp
610 615 620

Glu Lys Ala Val Ile Thr Val Gln Arg Pro Gly Arg Ile Pro Thr Ser
625 630 635 640

Ser Arg Cys Gly Asn Thr Ile Pro Asp Asp Asp Asn Gln Val Val Ser
645 650 655

Leu Ser Pro Gly Ser Arg Tyr Val Val Leu Pro Arg Pro Val Cys Phe
660 665 670

Glu Lys Gly Thr Asn Tyr Thr Val Arg Leu Glu Leu Pro Gln Tyr Thr
675 680 685

Ser Ser Asp Ser Asp Val Glu Ser Pro Tyr Thr Leu Ile Asp Ser Leu
690 695 700

Val Leu Met Pro Tyr Cys Lys Ser Leu Asp Ile Phe Thr Val Gly Gly
705 710 715 720

Ser Gly Asp Gly Val Val Thr Asn Ser Ala Trp Glu Thr Phe Gln Arg
725 730 735

Tyr Arg Cys Leu Glu Asn Ser Arg Ser Val Val Lys Thr Pro Met Thr
740 745 750

1241.22

Asp Val Cys Arg Asn Ile Ile Phe Ser Ile Ser Ala Leu Leu His Gln
755 760 765

Thr Gly Leu Ala Cys Glu Cys Asp Pro Gln Gly Ser Leu Ser Ser Val
770 775 780

Cys Asp Pro Asn Gly Gly Gln Cys Gln Cys Arg Pro Asn Val Val Gly
785 790 795 800

Arg Thr Cys Asn Arg Cys Ala Pro Gly Thr Phe Gly Phe Gly Pro Ser
805 810 815

Gly Cys Lys Pro Cys Glu Cys His Leu Gln Gly Ser Val Asn Ala Phe
820 825 830

Cys Asn Pro Val Thr Gly Gln Cys His Cys Phe Gln Gly Val Tyr Ala
835 840 845

Arg Gln Cys Asp Arg Cys Leu Pro Gly His Trp Gly Phe Pro Ser Cys
850 855 860

Gln Pro Cys Gln Cys Asn Gly His Ala Asp Asp Cys Asp Pro Val Thr
865 870 875 880

Gly Glu Cys Leu Asn Cys Gln Asp Tyr Thr Met Gly His Asn Cys Glu
885 890 895

Arg Cys Leu Ala Gly Tyr Tyr Gly Asp Pro Ile Ile Gly Ser Gly Asp
900 905 910

His Cys Arg Pro Cys Pro Cys Pro Asp Gly Pro Asp Ser Gly Arg Gln
915 920 925

Phe Ala Arg Ser Cys Tyr Gln Asp Pro Val Thr Leu Gln Leu Ala Cys
930 935 940

Val Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys Asp Asp Cys Ala Ser
945 950 955 960

Gly Tyr Phe Gly Asn Pro Ser Glu Val Gly Gly Ser Cys Gln Pro Cys
965 970 975

Gln Cys His Asn Asn Ile Asp Thr Thr Asp Pro Glu Ala Cys Asp Lys
980 985 990

Glu Thr Gly Arg Cys Leu Lys Cys Leu Tyr His Thr Glu Gly Glu His

1241.22

995	1000	1005
Cys Gln Phe Cys Arg Phe Gly Tyr Tyr Gly Asp Ala Leu Arg Gln Asp		
1010	1015	1020
Cys Arg Lys Cys Val Cys Asn Tyr Leu Gly Thr Val Gln Glu His Cys		
1025	1030	1035
Asn Gly Ser Asp Cys Gln Cys Asp Lys Ala Thr Gly Gln Cys Leu Cys		
1045	1050	1055
Leu Pro Asn Val Ile Gly Gln Asn Cys Asp Arg Cys Ala Pro Asn Thr		
1060	1065	1070
Trp Gln Leu Ala Ser Gly Thr Gly Cys Asp Pro Cys Asn Cys Asn Ala		
1075	1080	1085
Ala His Ser Phe Gly Pro Ser Cys Asn Glu Phe Thr Gly Gln Cys Gln		
1090	1095	1100
Cys Met Pro Gly Phe Gly Gly Arg Thr Cys Ser Glu Cys Gln Glu Leu		
1105	1110	1115
Phe Trp Gly Asp Pro Asp Val Glu Cys Arg Ala Cys Asp Cys Asp Pro		
1125	1130	1135
Arg Gly Ile Glu Thr Pro Gln Cys Asp Gln Ser Thr Gly Gln Cys Val		
1140	1145	1150
Cys Val Glu Gly Val Glu Gly Pro Arg Cys Asp Lys Cys Thr Arg Gly		
1155	1160	1165
Tyr Ser Gly Val Phe Pro Asp Cys Thr Pro Cys His Gln Cys Phe Ala		
1170	1175	1180
Leu Trp Asp Val Ile Ile Ala Glu Leu Thr Asn Arg Thr His Arg Phe		
1185	1190	1195
Leu Glu Lys Ala Lys Ala Leu Lys Ile Ser Gly Val Ile Gly Pro Tyr		
1205	1210	1215
Arg Glu Thr Val Asp Ser Val Glu Arg Lys Val Ser Glu Ile Lys Asp		
1220	1225	1230
Ile Leu Ala Gln Ser Pro Ala Ala Glu Pro Leu Lys Asn Ile Gly Asn		
1235	1240	1245
Leu Phe Glu Glu Ala Glu Lys Leu Ile Lys Asp Val Thr Glu Met Met		

1241.22

1250	1255	1260
Ala Gln Val Glu Val Lys Leu Ser Asp Thr Thr Ser Gln Ser Asn Ser		
1265	1270	1275
Thr Ala Lys Glu Leu Asp Ser Leu Gln Thr Glu Ala Glu Ser Leu Asp		1280
	1285	1290
Asn Thr Val Lys Glu Leu Ala Glu Gln Leu Glu Phe Ile Lys Asn Ser		1295
	1300	1305
Asp Ile Arg Gly Ala Leu Asp Ser Ile Thr Lys Tyr Phe Gln Met Ser		1310
	1315	1320
Leu Glu Ala Glu Glu Arg Val Asn Ala Ser Thr Thr Glu Pro Asn Ser		1325
	1330	1335
Thr Val Glu Gln Ser Ala Leu Met Arg Asp Arg Val Glu Asp Val Met		1340
1345	1350	1355
Met Glu Arg Glu Ser Gln Phe Lys Glu Lys Gln Glu Glu Gln Ala Arg		1360
	1365	1370
Leu Leu Asp Glu Leu Ala Gly Lys Leu Gln Ser Leu Asp Leu Ser Ala		1375
	1380	1385
Ala Ala Glu Met Thr Cys Gly Thr Pro Pro Gly Ala Ser Cys Ser Glu		1390
	1395	1400
Thr Glu Cys Gly Gly Pro Asn Cys Arg Thr Asp Glu Gly Glu Arg Lys		1405
	1410	1415
Cys Gly Gly Pro Gly Cys Gly Gly Leu Val Thr Val Ala His Asn Ala		1420
1425	1430	1435
Trp Gln Lys Ala Met Asp Leu Asp Gln Asp Val Leu Ser Ala Leu Ala		1440
	1445	1450
Glu Val Glu Gln Leu Ser Lys Met Val Ser Glu Ala Lys Leu Arg Ala		1455
	1460	1465
Asp Glu Ala Lys Gln Ser Ala Glu Asp Ile Leu Leu Lys Thr Asn Ala		1470
	1475	1480
Thr Lys Glu Lys Met Asp Lys Ser Asn Glu Glu Leu Arg Asn Leu Ile		1485
	1490	1495
		1500

1241.22

Lys Gln Ile Arg Asn Phe Leu Thr Gln Asp Ser Ala Asp Leu Asp Ser
1505 1510 1515 1520

Ile Glu Ala Val Ala Asn Glu Val Leu Lys Met Glu Met Pro Ser Thr
 1525 1530 1535

Pro Gln Gln Leu Gln Asn Leu Thr Glu Asp Ile Arg Glu Arg Val Glu
 1540 1545 1550

Ser Leu Ser Gln Val Glu Val Ile Leu Gln His Ser Ala Ala Asp Ile
 1555 1560 1565

Ala Arg Ala Glu Met Leu Leu Glu Glu Ala Lys Arg Ala Ser Lys Ser
 1570 1575 1580

Ala Thr Asp Val Lys Val Thr Ala Asp Met Val Lys Glu Ala Leu Glu
1585 1590 1595 1600

Glu Ala Glu Lys Ala Gln Val Ala Ala Glu Lys Ala Ile Lys Gln Ala
 1605 1610 1615

Asp Glu Asp Ile Gln Gly Thr Gln Asn Leu Leu Thr Ser Ile Glu Ser
 1620 1625 1630

Glu Thr Ala Ala Ser Glu Glu Thr Leu Phe Asn Ala Ser Gln Arg Ile
 1635 1640 1645

Ser Glu Leu Glu Arg Asn Val Glu Glu Leu Lys Arg Lys Ala Ala Gln
 1650 1655 1660

Asn Ser Gly Glu Ala Glu Tyr Ile Glu Lys Val Val Tyr Thr Val Lys
1665 1670 1675 1680

Gln Ser Ala Glu Asp Val Lys Lys Thr Leu Asp Gly Glu Leu Asp Glu
 1685 1690 1695

Lys Tyr Lys Lys Val Glu Asn Leu Ile Ala Lys Lys Thr Glu Glu Ser
 1700 1705 1710

Ala Asp Ala Arg Arg Lys Ala Glu Met Leu Gln Asn Glu Ala Lys Thr
 1715 1720 1725

Leu Leu Ala Gln Ala Asn Ser Lys Leu Gln Leu Leu Lys Asp Leu Glu
 1730 1735 1740

Arg Lys Tyr Glu Asp Asn Gln Arg Tyr Leu Glu Asp Lys Ala Gln Glu
1745 1750 1755 1760

1241.22

Leu Ala Arg Leu Glu Gly Glu Val Arg Ser Leu Leu Lys Asp Ile Ser

1765

1770

1775

Gln Lys Val Ala Val Tyr Ser Thr Cys Leu

1780

1785

<210> 77

<211> 585

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (27)..(335)

<400> 77

ctgagactga cctgcaggac gaaacc atg aag agc ctg atc ctt ctt gcc atc 53

Met Lys Ser Leu Ile Leu Leu Ala Ile

1

5

ctg gcc gcc tta gcg gta gta act ttg tgt tat gaa tca cat gaa agc 101

Leu Ala Ala Leu Ala Val Val Thr Leu Cys Tyr Glu Ser His Glu Ser

10

15

20

25

atg gaa tct tat gaa ctt aat ccc ttc att aac agg aga aat gca aat 149

Met Glu Ser Tyr Glu Leu Asn Pro Phe Ile Asn Arg Arg Asn Ala Asn

30

35

40

acc ttc ata tcc cct cag cag aga tgg aga gct aaa gtc caa gag agg 197

Thr Phe Ile Ser Pro Gln Gln Arg Trp Arg Ala Lys Val Gln Glu Arg

45

50

55

atc cga gaa cgc tct aag cct gtc cac gag ctc aat agg gaa gcc tgt 245

Ile Arg Glu Arg Ser Lys Pro Val His Glu Leu Asn Arg Glu Ala Cys

60

65

70

gat gac tac aga ctt tgc gaa cgc tac gcc atg gtt tat gga tac aat 293

Asp Asp Tyr Arg Leu Cys Glu Arg Tyr Ala Met Val Tyr Gly Tyr Asn

75

80

85

gct gcc tat aat cgc tac ttc agg aag cgc cga ggg acc aaa 335

1241.22

Ala Ala Tyr Asn Arg Tyr Phe Arg Lys Arg Arg Gly Thr Lys

90 95 100

tgagactgag ggaagaaaaa aaatctcttt ttttctggag gctggcacct gatTTTgtat 395
ccccctgtag cagcattact gaaatacata ggcttatata caatgcttct ttcctgtata 455
ttctcttgtc tggctgcacc cctttttccc gccccagat tgataagtaa tgaaagtgca 515
ctgcagtgag ggtcaaagga gagtcaacat atgtgattgt tccataataa acttctggtg 575
tgatactttc 585

<210> 78

<211> 103

<212> PRT

<213> Homo sapiens

<400> 78

Met Lys Ser Leu Ile Leu Leu Ala Ile Leu Ala Ala Leu Ala Val Val
1 5 10 15
Thr Leu Cys Tyr Glu Ser His Glu Ser Met Glu Ser Tyr Glu Leu Asn
20 25 30
Pro Phe Ile Asn Arg Arg Asn Ala Asn Thr Phe Ile Ser Pro Gln Gln
35 40 45
Arg Trp Arg Ala Lys Val Gln Glu Arg Ile Arg Glu Arg Ser Lys Pro
50 55 60
Val His Glu Leu Asn Arg Glu Ala Cys Asp Asp Tyr Arg Leu Cys Glu
65 70 75 80
Arg Tyr Ala Met Val Tyr Gly Tyr Asn Ala Ala Tyr Asn Arg Tyr Phe
85 90 95
Arg Lys Arg Arg Gly Thr Lys
100

<210> 79

<211> 1775

<212> DNA

<213> Homo sapiens

1241.22

<220>

<221> CDS

<222> (6)..(1148)

<400> 79

cagca atg cat ctc ctt gcg att ctg ttt tgt gct ctc tgg tct gca gtg 50

Met His Leu Leu Ala Ile Leu Phe Cys Ala Leu Trp Ser Ala Val

1 5 10 15

ttg gcc gag aac tcg gat gat tat gat ctc atg tat gtg aat ttg gac 98

Leu Ala Glu Asn Ser Asp Asp Tyr Asp Leu Met Tyr Val Asn Leu Asp

20 25 30

aac gaa ata gac aat gga ctc cat ccc act gag gac ccc acg ccg tgc 146

Asn Glu Ile Asp Asn Gly Leu His Pro Thr Glu Asp Pro Thr Pro Cys

35 40 45

gcc tgc ggt cag gag cac tcg gaa tgg gac aag ctc ttc atc atg ctg 194

Ala Cys Gly Gln Glu His Ser Glu Trp Asp Lys Leu Phe Ile Met Leu

50 55 60

gag aac tcg cag atg aga gag cgc atg ctg ctg caa gcc acg gac gac 242

Glu Asn Ser Gln Met Arg Glu Arg Met Leu Leu Gln Ala Thr Asp Asp

65 70 75

gtc ctg cgg ggc gag ctg cag agg ctg cgg gag gag ctg ggc cgg ctc 290

Val Leu Arg Gly Glu Leu Gln Arg Leu Arg Glu Glu Leu Gly Arg Leu

80 85 90 95

gcg gaa agc ctg gcg agg ccg tgc gcg ccg ggg gct ccc gca gag gcc 338

Ala Glu Ser Leu Ala Arg Pro Cys Ala Pro Gly Ala Pro Ala Glu Ala

100 105 110

agg ctg acc agt gct ctg gac gag ctg ctg cag gcg acc cgc gac gcg 386

Arg Leu Thr Ser Ala Leu Asp Glu Leu Leu Gln Ala Thr Arg Asp Ala

115 120 125

ggc cgc agg ctg gcg cgt atg gag ggc gcg gag gcg cag cgc cca gag 434

Gly Arg Arg Leu Ala Arg Met Glu Gly Ala Glu Ala Gln Arg Pro Glu

130 135 140

gag gcg ggg cgc gcc ctg gcc gcg gtg cta gag gag ctg cgg cag acg 482

1241.22

Glu Ala Gly Arg Ala Leu Ala Ala Val Leu Glu Glu Leu Arg Gln Thr	
145	150
cga gcc gac ctg cac gcg gtg cag ggc tgg gct gcc cgg agc tgg ctg	530
Arg Ala Asp Leu His Ala Val Gln Gly Trp Ala Ala Arg Ser Trp Leu	
160	165
ccg gca ggt tgt gaa aca gct att tta ttc cca atg cgt tcc aag aag	578
Pro Ala Gly Cys Glu Thr Ala Ile Leu Phe Pro Met Arg Ser Lys Lys	
180	185
att ttt gga agc gtg cat cca gtg aga cca atg agg ctt gag tct ttt	626
Ile Phe Gly Ser Val His Pro Val Arg Pro Met Arg Leu Glu Ser Phe	
195	200
agt gcc tgc att tgg gtc aaa gcc aca gat gta tta aac aaa acc atc	674
Ser Ala Cys Ile Trp Val Lys Ala Thr Asp Val Leu Asn Lys Thr Ile	
210	215
ctg ttt tcc tat ggc aca aag agg aat cca tat gaa atc cag ctg tat	722
Leu Phe Ser Tyr Gly Thr Lys Arg Asn Pro Tyr Glu Ile Gln Leu Tyr	
225	230
ctc agc tac caa tcc ata gtg ttt gtg gtg ggt gga gag gag aac aaa	770
Leu Ser Tyr Gln Ser Ile Val Phe Val Val Gly Gly Glu Glu Asn Lys	
240	245
ctg gtt gct gaa gcc atg gtt tcc ctg gga agg tgg acc cac ctg tgc	818
Leu Val Ala Glu Ala Met Val Ser Leu Gly Arg Trp Thr His Leu Cys	
260	265
ggc acc tgg aat tca gag gaa ggg ctc aca tcc ttg tgg gta aat ggt	866
Gly Thr Trp Asn Ser Glu Glu Gly Leu Thr Ser Leu Trp Val Asn Gly	
275	280
gaa ctg gcg gct acc act gtt gag atg gcc aca ggt cac att gtt cct	914
Glu Leu Ala Ala Thr Thr Val Glu Met Ala Thr Gly His Ile Val Pro	
290	295
gag gga gga atc ctg cag att ggc caa gaa aag aat ggc tgc tgt gtg	962
Glu Gly Gly Ile Leu Gln Ile Gly Gln Glu Lys Asn Gly Cys Cys Val	

1241.22
315

305	310		
ggt ggt ggc ttt gat gaa aca tta gcc ttc tct ggg aga ctc aca ggc			1010
Gly Gly Gly Phe Asp Glu Thr Leu Ala Phe Ser Gly Arg Leu Thr Gly			
320	325	330	335
ttc aat atc tgg gat agt gtt ctt agc aat gaa gag ata aga gag acc			1058
Phe Asn Ile Trp Asp Ser Val Leu Ser Asn Glu Glu Ile Arg Glu Thr			
340	345	350	
gga gga gca gag tct tgt cac atc cgg ggg aat att gtt ggg tgg gga			1106
Gly Gly Ala Glu Ser Cys His Ile Arg Gly Asn Ile Val Gly Trp Gly			
355	360	365	
gtc aca gag atc cag cca cat gga gga gct cag tat gtt tca			1148
Val Thr Glu Ile Gln Pro His Gly Gly Ala Gln Tyr Val Ser			
370	375	380	
taaatgttgt gaaactccac ttgaagccaa agaaagaaac tcacacttaa aacacatgcc			1208
agttgggaag gtctgaaaac tcagtgcata ataggaacac ttgagactaa tgaaagagag			1268
agttgagacc aatctttatt tgtactggcc aaatactgaa taaacagttg aaggaaagac			1328
attggaaaaa gcttttgagg ataatgttac tagactttat gccatggtgc tttcagttta			1388
atgctgtgtc tctgtcagat aaactctcaa ataattaaaa aggactgtat tgttgaacag			1448
agggacaatt gttttacttt tctttggtta attttgtttt ggccagagat gaattttaca			1508
ttggaagaat aacaaaataa gatttgttgt ccattgttca ttgttattgg tatgtacctt			1568
attacaaaaa aaatgatgaa aacatattta tactacaagg tgacttaaca actataaatg			1628
tagtttatgt gttataatcg aatgtcacgt ttttgagaag atagtcatat aagttatatt			1688
gcaaaaggga tttgtattaa ttttaagacta tttttgtaaa gctctactgt aaataaaata			1748
ttttataaaa ctaaaaaaaaa aaaaaaa			1775

<210> 80

<211> 381

<212> PRT

<213> Homo sapiens

<400> 80

Met His Leu Leu Ala Ile Leu Phe Cys Ala Leu Trp Ser Ala Val Leu

1

5

10

15

1241.22

Ala Glu Asn Ser Asp Asp Tyr Asp Leu Met Tyr Val Asn Leu Asp Asn
20 25 30

Glu Ile Asp Asn Gly Leu His Pro Thr Glu Asp Pro Thr Pro Cys Ala
35 40 45

Cys Gly Gln Glu His Ser Glu Trp Asp Lys Leu Phe Ile Met Leu Glu
50 55 60

Asn Ser Gln Met Arg Glu Arg Met Leu Leu Gln Ala Thr Asp Asp Val
65 70 75 80

Leu Arg Gly Glu Leu Gln Arg Leu Arg Glu Glu Leu Gly Arg Leu Ala
85 90 95

Glu Ser Leu Ala Arg Pro Cys Ala Pro Gly Ala Pro Ala Glu Ala Arg
100 105 110

Leu Thr Ser Ala Leu Asp Glu Leu Leu Gln Ala Thr Arg Asp Ala Gly
115 120 125

Arg Arg Leu Ala Arg Met Glu Gly Ala Glu Ala Gln Arg Pro Glu Glu
130 135 140

Ala Gly Arg Ala Leu Ala Ala Val Leu Glu Glu Leu Arg Gln Thr Arg
145 150 155 160

Ala Asp Leu His Ala Val Gln Gly Trp Ala Ala Arg Ser Trp Leu Pro
165 170 175

Ala Gly Cys Glu Thr Ala Ile Leu Phe Pro Met Arg Ser Lys Lys Ile
180 185 190

Phe Gly Ser Val His Pro Val Arg Pro Met Arg Leu Glu Ser Phe Ser
195 200 205

Ala Cys Ile Trp Val Lys Ala Thr Asp Val Leu Asn Lys Thr Ile Leu
210 215 220

Phe Ser Tyr Gly Thr Lys Arg Asn Pro Tyr Glu Ile Gln Leu Tyr Leu
225 230 235 240

Ser Tyr Gln Ser Ile Val Phe Val Val Gly Gly Glu Glu Asn Lys Leu
245 250 255

Val Ala Glu Ala Met Val Ser Leu Gly Arg Trp Thr His Leu Cys Gly
260 265 270

1241.22

Thr Trp Asn Ser Glu Glu Gly Leu Thr Ser Leu Trp Val Asn Gly Glu
275 280 285
Leu Ala Ala Thr Thr Val Glu Met Ala Thr Gly His Ile Val Pro Glu
290 295 300
Gly Gly Ile Leu Gln Ile Gly Gln Glu Lys Asn Gly Cys Cys Val Gly
305 310 315 320
Gly Gly Phe Asp Glu Thr Leu Ala Phe Ser Gly Arg Leu Thr Gly Phe
325 330 335
Asn Ile Trp Asp Ser Val Leu Ser Asn Glu Glu Ile Arg Glu Thr Gly
340 345 350
Gly Ala Glu Ser Cys His Ile Arg Gly Asn Ile Val Gly Trp Gly Val
355 360 365
Thr Glu Ile Gln Pro His Gly Gly Ala Gln Tyr Val Ser
370 375 380

<210> 81

<211> 2312

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (146)..(1192)

<400> 81

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ctccgctccg cccgcagtgc caacc atg acc gcc gcc agt atg ggc ccc gtc 172
Met Thr Ala Ala Ser Met Gly Pro Val
1 5
cgc gtc gcc ttc gtg gtc ctc ctc gcc ctc tgc agc cgg ccg gcc gtc 220
Arg Val Ala Phe Val Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val
10 15 20 25
ggc cag aac tgc agc ggg ccg tgc cgg tgc ccg gac gag ccg gcg ccg 268

1241.22

Gly	Gln	Asn	Cys	Ser	Gly	Pro	Cys	Arg	Cys	Pro	Asp	Glu	Pro	Ala	Pro		
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cgc	tgc	ccg	gcg	ggc	gtg	agc	ctc	gtg	ctg	gac	ggc	tgc	ggc	tgc	tgc	316	
Arg	Cys	Pro	Ala	Gly	Val	Ser	Leu	Val	Leu	Asp	Gly	Cys	Gly	Cys	Cys		
			45					50						55			
cgc	gtc	tgc	gcc	aag	cag	ctg	ggc	gag	ctg	tgc	acc	gag	cgc	gac	ccc	364	
Arg	Val	Cys	Ala	Lys	Gln	Leu	Gly	Glu	Leu	Cys	Thr	Glu	Arg	Asp	Pro		
		60						65						70			
tgc	gac	ccg	cac	aag	ggc	ctc	ttc	tgt	gac	ttc	ggc	tcc	ccg	gcc	aac	412	
Cys	Asp	Pro	His	Lys	Gly	Leu	Phe	Cys	Asp	Phe	Gly	Ser	Pro	Ala	Asn		
		75					80							85			
cgc	aag	atc	ggc	gtg	tgc	acc	gcc	aaa	gat	ggt	gct	ccc	tgc	atc	ttc	460	
Arg	Lys	Ile	Gly	Val	Cys	Thr	Ala	Lys	Asp	Gly	Ala	Pro	Cys	Ile	Phe		
	90					95				100				105			
ggt	ggt	acg	gtg	tac	cgc	agc	gga	gag	tcc	ttc	cag	agc	agc	tgc	aag	508	
Gly	Gly	Thr	Val	Tyr	Arg	Ser	Gly	Glu	Ser	Phe	Gln	Ser	Ser	Cys	Lys		
				110						115				120			
tac	cag	tgc	acg	tgc	ctg	gac	ggg	gcg	gtg	ggc	tgc	atg	ccc	ctg	tgc	556	
Tyr	Gln	Cys	Thr	Cys	Leu	Asp	Gly	Ala	Val	Gly	Cys	Met	Pro	Leu	Cys		
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agc	atg	gac	gtt	cgt	ctg	ccc	agc	cct	gac	tgc	ccc	ttc	ccg	agg	agg	604	
Ser	Met	Asp	Val	Arg	Leu	Pro	Ser	Pro	Asp	Cys	Pro	Phe	Pro	Arg	Arg		
			140							145				150			
gtc	aag	ctg	ccc	ggg	aaa	tgc	tgc	gag	gag	tgg	gtg	tgt	gac	gag	ccc	652	
Val	Lys	Leu	Pro	Gly	Lys	Cys	Cys	Glu	Glu	Trp	Val	Cys	Asp	Glu	Pro		
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aag	gac	caa	acc	gtg	gtt	ggg	cct	gcc	ctc	gcg	gct	tac	cga	ctg	gaa	700	
Lys	Asp	Gln	Thr	Val	Val	Gly	Pro	Ala	Leu	Ala	Ala	Tyr	Arg	Leu	Glu		
		170				175								180			
gac	acg	ttt	ggc	cca	gac	cca	act	atg	att	aga	gcc	aac	tgc	ctg	gtc	748	
Asp	Thr	Phe	Gly	Pro	Asp	Pro	Thr	Met	Ile	Arg	Ala	Asn	Cys	Leu	Val		

1241.22

190	195	200	
cag acc aca gag tgg agc gcc tgt tcc aag acc tgt ggg atg ggc atc			796
Gln Thr Thr Glu Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile			
205	210	215	
tcc acc cgg gtt acc aat gac aac gcc tcc tgc agg cta gag aag cag			844
Ser Thr Arg Val Thr Asn Asp Asn Ala Ser Cys Arg Leu Glu Lys Gln			
220	225	230	
agc cgc ctg tgc atg gtc agg cct tgc gaa gct gac ctg gaa gag aac			892
Ser Arg Leu Cys Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn			
235	240	245	
att aag aag ggc aaa aag tgc atc cgt act ccc aaa atc tcc aag cct			940
Ile Lys Lys Gly Lys Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro			
250	255	260	265
atc aag ttt gag ctt tct ggc tgc acc agc atg aag aca tac cga gct			988
Ile Lys Phe Glu Leu Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala			
270	275	280	
aaa ttc tgt gga gta tgt acc gac ggc cga tgc tgc acc ccc cac aga			1036
Lys Phe Cys Gly Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg			
285	290	295	
acc acc acc ctg ccg gtg gag ttc aag tgc cct gac ggc gag gtc atg			1084
Thr Thr Thr Leu Pro Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met			
300	305	310	
aag aag aac atg atg ttc atc aag acc tgt gcc tgc cat tac aac tgt			1132
Lys Lys Asn Met Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys			
315	320	325	
ccc gga gac aat gac atc ttt gaa tcg ctg tac tac agg aag atg tac			1180
Pro Gly Asp Asn Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr			
330	335	340	345
gga gac atg gca tgaagccaga gagttagaga cattaactca ttagactgga			1232
Gly Asp Met Ala			
acttgaactg attcacatct cttttttccg taaaaatgat ttcagtagca caagttattt			1292
aaatctgttt ttctaactgg gggaaaagat tcccacccaa ttcaaaacat tgtgccatgt			1352

1241.22

caaacaaata gtctatcttc cccagacact ggtttgaaga atgttaagac ttgacagtgg 1412
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<210> 82

<211> 349

<212> PRT

<213> Homo sapiens

<400> 82

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Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser

35 40 45

Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu

50 55 60

Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu

65 70 75 80

1241.22

Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr
85 90 95
Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser
100 105 110
Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp
115 120 125
Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro
130 135 140
Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys
145 150 155 160
Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly
165 170 175
Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro
180 185 190
Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala
195 200 205
Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp
210 215 220
Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg
225 230 235 240
Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys
245 250 255
Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly
260 265 270
Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr
275 280 285
Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu
290 295 300
Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile
305 310 315 320
Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe

1241.22

325 330 335

Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala

340 345

<210> 83

<211> 2954

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (173)..(1525)

<400> 83

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taaccgggtc aatgtgtgga atattggggg gctcggctgc agacttggcc aa atg gac 178

Met Asp

1

ggg act att aag gag gct ctg tcg gtg gtg agc gac gac cag tcc ctc 226

Gly Thr Ile Lys Glu Ala Leu Ser Val Val Ser Asp Asp Gln Ser Leu

5 10 15

ttt gac tca gcg tac gga gcg gca gcc cat ctc ccc aag gcc gac atg 274

Phe Asp Ser Ala Tyr Gly Ala Ala Ala His Leu Pro Lys Ala Asp Met

20 25 30

act gcc tcg ggg agt cct gac tac ggg cag ccc cac aag atc aac ccc 322

Thr Ala Ser Gly Ser Pro Asp Tyr Gly Gln Pro His Lys Ile Asn Pro

35 40 45 50

ctc cca cca cag cag gag tgg atc aat cag cca gtg agg gtc aac gtc 370

Leu Pro Pro Gln Gln Glu Trp Ile Asn Gln Pro Val Arg Val Asn Val

55 60 65

aag cgg gag tat gac cac atg aat gga tcc agg gag tct ccg gtg gac 418

Lys Arg Glu Tyr Asp His Met Asn Gly Ser Arg Glu Ser Pro Val Asp

70 75 80

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Cys Ser Val Ser Lys Cys Ser Lys Leu Val Gly Gly Gly Glu Ser Asn																	
85 90 95																	
ccc atg aac tac aac agc tat atg gac gag aag aat ggc ccc cct cct	514																
Pro Met Asn Tyr Asn Ser Tyr Met Asp Glu Lys Asn Gly Pro Pro Pro																	
100 105 110																	
ccc aac atg acc acc aac gag agg aga gtc atc gtc ccc gca gac ccc	562																
Pro Asn Met Thr Thr Asn Glu Arg Arg Val Ile Val Pro Ala Asp Pro																	
115 120 125 130																	
aca ctg tgg aca cag gag cat gtg agg caa tgg ctg gag tgg gcc ata	610																
Thr Leu Trp Thr Gln Glu His Val Arg Gln Trp Leu Glu Trp Ala Ile																	
135 140 145																	
aag gag tac agc ttg atg gag atc gac aca tcc ttt ttc cag aac atg	658																
Lys Glu Tyr Ser Leu Met Glu Ile Asp Thr Ser Phe Phe Gln Asn Met																	
150 155 160																	
gat ggc aag gaa ctg tgt aaa atg aac aag gag gac ttc ctc cgc gcc	706																
Asp Gly Lys Glu Leu Cys Lys Met Asn Lys Glu Asp Phe Leu Arg Ala																	
165 170 175																	
acc acc ctc tac aac acg gaa gtg ctg ttg tca cac ctc agt tac ctc	754																
Thr Thr Leu Tyr Asn Thr Glu Val Leu Leu Ser His Leu Ser Tyr Leu																	
180 185 190																	
agg gaa agt tca ctg ctg gcc tat aat aca acc tcc cac acc gac caa	802																
Arg Glu Ser Ser Leu Leu Ala Tyr Asn Thr Thr Ser His Thr Asp Gln																	
195 200 205 210																	
tcc tca cga ttg agt gtc aaa gaa gac cct tct tat gac tca gtc aga	850																
Ser Ser Arg Leu Ser Val Lys Glu Asp Pro Ser Tyr Asp Ser Val Arg																	
215 220 225																	
aga gga gct tgg ggc aat aac atg aat tct ggc ctc aac aaa agt cct	898																
Arg Gly Ala Trp Gly Asn Asn Met Asn Ser Gly Leu Asn Lys Ser Pro																	
230 235 240																	
ccc ctt gga ggg gca caa acg atc agt aag aat aca gag caa cgg ccc	946																
Pro Leu Gly Gly Ala Gln Thr Ile Ser Lys Asn Thr Glu Gln Arg Pro																	

1241.22

245	250	255	
cag cca gat ccg tat cag atc ctg ggc ccg acc agc agt cgc cta gcc			994
Gln Pro Asp Pro Tyr Gln Ile Leu Gly Pro Thr Ser Ser Arg Leu Ala			
260	265	270	
aac cct gga agc ggg cag atc cag ctg tgg caa ttc ctc ctg gag ctg			1042
Asn Pro Gly Ser Gly Gln Ile Gln Leu Trp Gln Phe Leu Leu Glu Leu			
275	280	285	290
ctc tcc gac agc gcc aac gcc agc tgt atc acc tgg gag ggg acc aac			1090
Leu Ser Asp Ser Ala Asn Ala Ser Cys Ile Thr Trp Glu Gly Thr Asn			
295	300	305	
ggg gag ttc aaa atg acg gac ccc gat gag gtg gcc agg cgc tgg ggc			1138
Gly Glu Phe Lys Met Thr Asp Pro Asp Glu Val Ala Arg Arg Trp Gly			
310	315	320	
gag cgg aaa agc aag ccc aac atg aat tac gac aag ctg agc cgg gcc			1186
Glu Arg Lys Ser Lys Pro Asn Met Asn Tyr Asp Lys Leu Ser Arg Ala			
325	330	335	
ctc cgt tat tac tat gat aaa aac att atg acc aaa gtg cac ggc aaa			1234
Leu Arg Tyr Tyr Tyr Asp Lys Asn Ile Met Thr Lys Val His Gly Lys			
340	345	350	
aga tat gct tac aaa ttt gac ttc cac ggc att gcc cag gct ctg cag			1282
Arg Tyr Ala Tyr Lys Phe Asp Phe His Gly Ile Ala Gln Ala Leu Gln			
355	360	365	370
cca cat ccg acc gag tcg tcc atg tac aag tac cct tct gac atc tcc			1330
Pro His Pro Thr Glu Ser Ser Met Tyr Lys Tyr Pro Ser Asp Ile Ser			
375	380	385	
tac atg cct tcc caa cat gcc cac cag cag aag gtg aac ttt gtc cct			1378
Tyr Met Pro Ser Gln His Ala His Gln Gln Lys Val Asn Phe Val Pro			
390	395	400	
ccc cat cca tcc tcc atg cct gtc act tcc tcc agc ttc ttt gga gcc			1426
Pro His Pro Ser Ser Met Pro Val Thr Ser Ser Ser Phe Phe Gly Ala			
405	410	415	

1241.22

gca tca caa tac tgg acc tcc acg ggg gga atc tac ccc aac ccc aac 1474
Ala Ser Gln Tyr Trp Thr Ser Thr Gly Gly Ile Tyr Pro Asn Pro Asn
420 425 430

gtc ccc cgc cat cct aac acc cac gtg cct tca cac tta ggc agc tac 1522
Val Pro Arg His Pro Asn Thr His Val Pro Ser His Leu Gly Ser Tyr
435 440 445 450

tac tagaagctta ctcatcagtg gccttctagc tgaagcccat cctgcacact 1575
Tyr

tactggatgc tttggactca acaggacata tgtggccttg aaggggaagac aaaactggat 1635
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1241.22

<210> 84

<211> 451

<212> PRT

<213> Homo sapiens

<400> 84

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Asp Met Thr Ala Ser Gly Ser Pro Asp Tyr Gly Gln Pro His Lys Ile
35 40 45
Asn Pro Leu Pro Pro Gln Gln Glu Trp Ile Asn Gln Pro Val Arg Val
50 55 60
Asn Val Lys Arg Glu Tyr Asp His Met Asn Gly Ser Arg Glu Ser Pro
65 70 75 80
Val Asp Cys Ser Val Ser Lys Cys Ser Lys Leu Val Gly Gly Gly Glu
85 90 95
Ser Asn Pro Met Asn Tyr Asn Ser Tyr Met Asp Glu Lys Asn Gly Pro
100 105 110
Pro Pro Pro Asn Met Thr Thr Asn Glu Arg Arg Val Ile Val Pro Ala
115 120 125
Asp Pro Thr Leu Trp Thr Gln Glu His Val Arg Gln Trp Leu Glu Trp
130 135 140
Ala Ile Lys Glu Tyr Ser Leu Met Glu Ile Asp Thr Ser Phe Phe Gln
145 150 155 160
Asn Met Asp Gly Lys Glu Leu Cys Lys Met Asn Lys Glu Asp Phe Leu
165 170 175
Arg Ala Thr Thr Leu Tyr Asn Thr Glu Val Leu Leu Ser His Leu Ser
180 185 190
Tyr Leu Arg Glu Ser Ser Leu Leu Ala Tyr Asn Thr Thr Ser His Thr
195 200 205
Asp Gln Ser Ser Arg Leu Ser Val Lys Glu Asp Pro Ser Tyr Asp Ser

1241.22

210	215	220
Val Arg Arg Gly Ala Trp	Gly Asn Asn Met Asn Ser Gly Leu Asn Lys	
225	230	235
Ser Pro Pro Leu Gly Gly Ala Gln Thr Ile Ser Lys Asn Thr Glu Gln		240
245	250	255
Arg Pro Gln Pro Asp Pro Tyr Gln Ile Leu Gly Pro Thr Ser Ser Arg		
260	265	270
Leu Ala Asn Pro Gly Ser Gly Gln Ile Gln Leu Trp Gln Phe Leu Leu		
275	280	285
Glu Leu Leu Ser Asp Ser Ala Asn Ala Ser Cys Ile Thr Trp Glu Gly		
290	295	300
Thr Asn Gly Glu Phe Lys Met Thr Asp Pro Asp Glu Val Ala Arg Arg		
305	310	315
Trp Gly Glu Arg Lys Ser Lys Pro Asn Met Asn Tyr Asp Lys Leu Ser		
325	330	335
Arg Ala Leu Arg Tyr Tyr Tyr Asp Lys Asn Ile Met Thr Lys Val His		
340	345	350
Gly Lys Arg Tyr Ala Tyr Lys Phe Asp Phe His Gly Ile Ala Gln Ala		
355	360	365
Leu Gln Pro His Pro Thr Glu Ser Ser Met Tyr Lys Tyr Pro Ser Asp		
370	375	380
Ile Ser Tyr Met Pro Ser Gln His Ala His Gln Gln Lys Val Asn Phe		
385	390	395
Val Pro Pro His Pro Ser Ser Met Pro Val Thr Ser Ser Ser Phe Phe		
405	410	415
Gly Ala Ala Ser Gln Tyr Trp Thr Ser Thr Gly Gly Ile Tyr Pro Asn		
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Ser Tyr Tyr		
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1241.22

<210> 85

<211> 1817

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2)..(361)

<400> 85

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Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val Val
      20             25             30
cct tct gga gag gag cag aga tac acg tgc cat gtg cag cat gag ggg 145
Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His Glu Gly
      35             40             45
cta ccc gag ccc gtc acc ctg aga tgg aag ccg gct tcc cag ccc acc 193
Leu Pro Glu Pro Val Thr Leu Arg Trp Lys Pro Ala Ser Gln Pro Thr
      50             55             60
atc ccc atc gtg ggc atc att gct ggc ctg gtt ctc ctt gga tct gtg 241
Ile Pro Ile Val Gly Ile Ile Ala Gly Leu Val Leu Leu Gly Ser Val
      65             70             75             80
gtc tct gga gct gtg gtt gct gct gtg ata tgg agg aag aag agc tca 289
Val Ser Gly Ala Val Val Ala Ala Val Ile Trp Arg Lys Lys Ser Ser
      85             90             95
ggg gga aaa gga ggg agc tac tct aag gct gag tgg agc gac agt gcc 337
Gly Gly Lys Gly Gly Ser Tyr Ser Lys Ala Glu Trp Ser Asp Ser Ala
      100            105            110
cag ggg tct gag tct cac agc ttg taaagcctga gacagctgcc ttgtgtgcga 391
Gln Gly Ser Glu Ser His Ser Leu
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115

120

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ctttataaga agaggaaaag agaactgagc tagcatgccc agcccacaga gagcctccac 1351
tagagtgatg ctaagtggaa atgtgaggtg cagctgccac agagggcccc caccagggaa 1411
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gcaaagccac aggcacgggg ctacctgagc cttgggggcc caatccctgc tccagtgtgt 1651
ccgtgaggca gcacacgaag tcaaaagaga ttattctctt cccacagata cttttctct 1711
cccatgacct ttaacagca tctgcttcat tcccctcacc ttcccaggct gatctgaggt 1771
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<210> 86

<211> 120

<212> PRT

<213> Homo sapiens

<400> 86

Gln Gln Asp Gly Glu Gly His Thr Gln Asp Thr Glu Leu Val Glu Thr

1241.22

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Arg	Pro	Ala	Gly
Asp	Gly	Thr	Phe
Gln	Lys	Trp	Ala
Ala	Val	Val	Val
20	25	30	
Pro	Ser	Gly	Glu
Glu	Gln	Arg	Tyr
Thr	Cys	His	Val
Gln	His	Glu	Gly
35	40	45	
Leu	Pro	Glu	Pro
Val	Thr	Leu	Arg
Trp	Lys	Pro	Ala
Ser	Gln	Pro	Thr
50	55	60	
Ile	Pro	Ile	Val
Gly	Ile	Ile	Ala
Gly	Leu	Val	Leu
Leu	Gly	Ser	Val
65	70	75	80
Val	Ser	Gly	Ala
Val	Val	Ala	Ala
Val	Ile	Trp	Arg
Lys	Lys	Ser	Ser
85	90	95	
Gly	Gly	Lys	Gly
Gly	Ser	Tyr	Ser
Lys	Ala	Glu	Trp
Ser	Asp	Ser	Ala
100	105	110	
Gln	Gly	Ser	Glu
Ser	His	Ser	Leu
115	120		

<210> 87

<211> 2876

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76)..(1281)

<400> 87

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tctgagaact tcagg atg cag atg tct cca gcc ctc acc tgc cta gtc ctg 111
      Met Gln Met Ser Pro Ala Leu Thr Cys Leu Val Leu
      1           5           10
ggc ctg gcc ctt gtc ttt ggt gaa ggg tct gct gtg cac cat ccc cca 159
Gly Leu Ala Leu val Phe Gly Glu Gly Ser Ala Val His His Pro Pro
      15           20           25
tcc tac gtg gcc cac ctg gcc tca gac ttc ggg gtg agg gtg ttt cag 207

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1241.22

Ser Tyr Val Ala His Leu Ala Ser Asp Phe Gly Val Arg Val Phe Gln	
30 35 40	
cag gtg gcg cag gcc tcc aag gac cgc aac gtg gtt ttc tca ccc tat	255
Gln Val Ala Gln Ala Ser Lys Asp Arg Asn Val Val Phe Ser Pro Tyr	
45 50 55 60	
ggg gtg gcc tcg gtg ttg gcc atg ctc cag ctg aca aca gga gga gaa	303
Gly Val Ala Ser Val Leu Ala Met Leu Gln Leu Thr Thr Gly Gly Glu	
65 70 75	
acc cag cag cag att caa gca gct atg gga ttc aag att gat gac aag	351
Thr Gln Gln Gln Ile Gln Ala Ala Met Gly Phe Lys Ile Asp Asp Lys	
80 85 90	
ggc atg gcc ccc gcc ctc cgg cat ctg tac aag gag ctc atg ggg cca	399
Gly Met Ala Pro Ala Leu Arg His Leu Tyr Lys Glu Leu Met Gly Pro	
95 100 105	
tgg aac aag gat gag atc agc acc aca gac gcg atc ttc gtc cag cgg	447
Trp Asn Lys Asp Glu Ile Ser Thr Thr Asp Ala Ile Phe Val Gln Arg	
110 115 120	
gat ctg aag ctg gtc cag ggc ttc atg ccc cac ttc ttc agg ctg ttc	495
Asp Leu Lys Leu Val Gln Gly Phe Met Pro His Phe Phe Arg Leu Phe	
125 130 135 140	
cgg agc acg gtc aag caa gtg gac ttt tca gag gtg gag aga gcc aga	543
Arg Ser Thr Val Lys Gln Val Asp Phe Ser Glu Val Glu Arg Ala Arg	
145 150 155	
ttc atc atc aat gac tgg gtg aag aca cac aca aaa ggt atg atc agc	591
Phe Ile Ile Asn Asp Trp Val Lys Thr His Thr Lys Gly Met Ile Ser	
160 165 170	
aac ttg ctt ggg aaa gga gcc gtg gac cag ctg aca cgg ctg gtg ctg	639
Asn Leu Leu Gly Lys Gly Ala Val Asp Gln Leu Thr Arg Leu Val Leu	
175 180 185	
gtg aat gcc ctc tac ttc aac ggc cag tgg aag act ccc ttc ccc gac	687
Val Asn Ala Leu Tyr Phe Asn Gly Gln Trp Lys Thr Pro Phe Pro Asp	
190 195 200	

1241.22

atatatatat tttaaataata cttaaataata tttttctaata atcttttaaat atatatatat 2811
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<210> 88

<211> 402

<212> PRT

<213> Homo sapiens

<400> 88

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His Leu Ala Ser Asp Phe Gly Val Arg Val Phe Gln Gln Val Ala Gln
35 40 45
Ala Ser Lys Asp Arg Asn Val Val Phe Ser Pro Tyr Gly Val Ala Ser
50 55 60
Val Leu Ala Met Leu Gln Leu Thr Thr Gly Gly Glu Thr Gln Gln Gln
65 70 75 80
Ile Gln Ala Ala Met Gly Phe Lys Ile Asp Asp Lys Gly Met Ala Pro
85 90 95
Ala Leu Arg His Leu Tyr Lys Glu Leu Met Gly Pro Trp Asn Lys Asp
100 105 110
Glu Ile Ser Thr Thr Asp Ala Ile Phe Val Gln Arg Asp Leu Lys Leu
115 120 125
Val Gln Gly Phe Met Pro His Phe Phe Arg Leu Phe Arg Ser Thr Val
130 135 140
Lys Gln Val Asp Phe Ser Glu Val Glu Arg Ala Arg Phe Ile Ile Asn
145 150 155 160
Asp Trp Val Lys Thr His Thr Lys Gly Met Ile Ser Asn Leu Leu Gly
165 170 175
Lys Gly Ala Val Asp Gln Leu Thr Arg Leu Val Leu Val Asn Ala Leu

1241.22

180	185	190	
Tyr Phe Asn Gly Gln Trp Lys Thr Pro Phe Pro Asp Ser Ser Thr His			
195	200	205	
Arg Arg Leu Phe His Lys Ser Asp Gly Ser Thr Val Ser Val Pro Met			
210	215	220	
Met Ala Gln Thr Asn Lys Phe Asn Tyr Thr Glu Phe Thr Thr Pro Asp			
225	230	235	240
Gly His Tyr Tyr Asp Ile Leu Glu Leu Pro Tyr His Gly Asp Thr Leu			
245	250	255	
Ser Met Phe Ile Ala Ala Pro Tyr Glu Lys Glu Val Pro Leu Ser Ala			
260	265	270	
Leu Thr Asn Ile Leu Ser Ala Gln Leu Ile Ser His Trp Lys Gly Asn			
275	280	285	
Met Thr Arg Leu Pro Arg Leu Leu Val Leu Pro Lys Phe Ser Leu Glu			
290	295	300	
Thr Glu Val Asp Leu Arg Lys Pro Leu Glu Asn Leu Gly Met Thr Asp			
305	310	315	320
Met Phe Arg Gln Phe Gln Ala Asp Phe Thr Ser Leu Ser Asp Gln Glu			
325	330	335	
Pro Leu His Val Ala Gln Ala Leu Gln Lys Val Lys Ile Glu Val Asn			
340	345	350	
Glu Ser Gly Thr Val Ala Ser Ser Ser Thr Ala Val Ile Val Ser Ala			
355	360	365	
Arg Met Ala Pro Glu Glu Ile Ile Met Asp Arg Pro Phe Leu Phe Val			
370	375	380	
Val Arg His Asn Pro Thr Gly Thr Val Leu Phe Met Gly Gln Val Met			
385	390	395	400
Glu Pro			

<210> 89

<211> 1412

1241.22

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (52)..(1341)

<400> 89

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                                         Met Ser
                                         1
ttc acc act cgc tcc acc ttc tcc acc aac tac cgg tcc ctg ggc tct 105
Phe Thr Thr Arg Ser Thr Phe Ser Thr Asn Tyr Arg Ser Leu Gly Ser
      5              10              15
gtc cag gcg ccc agc tac ggc gcc cgg ccg gtc agc agc gcg gcc agc 153
Val Gln Ala Pro Ser Tyr Gly Ala Arg Pro Val Ser Ser Ala Ala Ser
      20              25              30
gtc tat gca ggc gct ggg ggc tct ggt tcc cgg atc tcc gtg tcc cgc 201
Val Tyr Ala Gly Ala Gly Gly Ser Gly Ser Arg Ile Ser Val Ser Arg
      35              40              45              50
tcc acc agc ttc agg ggc ggc atg ggg tcc ggg ggc ctg gcc acc ggg 249
Ser Thr Ser Phe Arg Gly Gly Met Gly Ser Gly Gly Leu Ala Thr Gly
      55              60              65
ata gcc ggg ggt ctg gca gga atg gga ggc atc cag aac gag aag gag 297
Ile Ala Gly Gly Leu Ala Gly Met Gly Gly Ile Gln Asn Glu Lys Glu
      70              75              80
acc atg caa agc ctg aac gac cgc ctg gcc tct tac ctg gac aga gtg 345
Thr Met Gln Ser Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp Arg Val
      85              90              95
agg agc ctg gag acc gag aac cgg agg ctg gag agc aaa atc cgg gag 393
Arg Ser Leu Glu Thr Glu Asn Arg Arg Leu Glu Ser Lys Ile Arg Glu
      100             105             110
cac ttg gag aag aag gga ccc cag gtc aga gac tgg agc cat tac ttc 441
His Leu Glu Lys Lys Gly Pro Gln Val Arg Asp Trp Ser His Tyr Phe
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1241.22

115	120	125	130	
aag atc atc gag gac ctg agg gct cag atc ttc gca aat act gtg gac				489
Lys Ile Ile Glu Asp Leu Arg Ala Gln Ile Phe Ala Asn Thr Val Asp				
	135	140	145	
aat gcc cgc atc gtt ctg cag att gac aat gcc cgt ctt gct gct gat				537
Asn Ala Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu Ala Ala Asp				
	150	155	160	
gac ttt aga gtc aag tat gag aca gag ctg gcc atg cgc cag tct gtg				585
Asp Phe Arg Val Lys Tyr Glu Thr Glu Leu Ala Met Arg Gln Ser Val				
	165	170	175	
gag aac gac atc cat ggg ctc cgc aag gtc att gat gac acc aat atc				633
Glu Asn Asp Ile His Gly Leu Arg Lys Val Ile Asp Asp Thr Asn Ile				
	180	185	190	
aca cga ctg cag ctg gag aca gag atc gag gct ctc aag gag gag ctg				681
Thr Arg Leu Gln Leu Glu Thr Glu Ile Glu Ala Leu Lys Glu Glu Leu				
195	200	205	210	
ctc ttc atg aag aag aac cac gaa gag gaa gta aaa ggc cta caa gcc				729
Leu Phe Met Lys Lys Asn His Glu Glu Glu Val Lys Gly Leu Gln Ala				
	215	220	225	
cag att gcc agc tct ggg ttg acc gtg gag gta gat gcc ccc aaa tct				777
Gln Ile Ala Ser Ser Gly Leu Thr Val Glu Val Asp Ala Pro Lys Ser				
	230	235	240	
cag gac ctc gcc aag atc atg gca gac atc cgg gcc caa tat gac gag				825
Gln Asp Leu Ala Lys Ile Met Ala Asp Ile Arg Ala Gln Tyr Asp Glu				
	245	250	255	
ctg gct cgg aag aac cga gag gag cta gac aag tac tgg tct cag cag				873
Leu Ala Arg Lys Asn Arg Glu Glu Leu Asp Lys Tyr Trp Ser Gln Gln				
	260	265	270	
att gag gag agc acc aca gtg gtc acc aca cag tct gct gag gtt gga				921
Ile Glu Glu Ser Thr Thr Val Val Thr Thr Gln Ser Ala Glu Val Gly				
275	280	285	290	

1241.22

gct gct gag acg acg ctc aca gag ctg aga cgt aca gtc cag tcc ttg	969
Ala Ala Glu Thr Thr Leu Thr Glu Leu Arg Arg Thr Val Gln Ser Leu	
295 300 305	
gag atc gac ctg gac tcc atg aga aat ctg aag gcc agc ttg gag aac	1017
Glu Ile Asp Leu Asp Ser Met Arg Asn Leu Lys Ala Ser Leu Glu Asn	
310 315 320	
agc ctg agg gag gtg gag gcc cgc tac gcc cta cag atg gag cag ctc	1065
Ser Leu Arg Glu Val Glu Ala Arg Tyr Ala Leu Gln Met Glu Gln Leu	
325 330 335	
aac ggg atc ctg ctg cac ctt gag tca gag ctg gca cag acc cgg gca	1113
Asn Gly Ile Leu Leu His Leu Glu Ser Glu Leu Ala Gln Thr Arg Ala	
340 345 350	
gag gga cag cgc cag gcc cag gag tat gag gcc ctg ctg aac atc aag	1161
Glu Gly Gln Arg Gln Ala Gln Glu Tyr Glu Ala Leu Leu Asn Ile Lys	
355 360 365 370	
gtc aag ctg gag gct gag atc gcc acc tac cgc cgc ctg ctg gaa gat	1209
Val Lys Leu Glu Ala Glu Ile Ala Thr Tyr Arg Arg Leu Leu Glu Asp	
375 380 385	
ggc gag gac ttt aat ctt ggt gat gcc ttg gac agc agc aac tcc atg	1257
Gly Glu Asp Phe Asn Leu Gly Asp Ala Leu Asp Ser Ser Asn Ser Met	
390 395 400	
caa acc atc caa aag acc acc acc cgc cgg ata gtg gat ggc aaa gtg	1305
Gln Thr Ile Gln Lys Thr Thr Thr Arg Arg Ile Val Asp Gly Lys Val	
405 410 415	
gtg tct gag acc aat gac acc aaa gtt ctg agg cat taagccagca	1351
Val Ser Glu Thr Asn Asp Thr Lys Val Leu Arg His	
420 425 430	
gaagcagggt accctttggg gagcaggagg ccaataaaaa gttcagagtt cattggatgt	1411
c	1412

<210> 90

<211> 430

1241.22

<212> PRT

<213> Homo sapiens

<400> 90

Met Ser Phe Thr Thr Arg Ser Thr Phe Ser Thr Asn Tyr Arg Ser Leu
1 5 10 15
Gly Ser Val Gln Ala Pro Ser Tyr Gly Ala Arg Pro Val Ser Ser Ala
20 25 30
Ala Ser Val Tyr Ala Gly Ala Gly Gly Ser Gly Ser Arg Ile Ser Val
35 40 45
Ser Arg Ser Thr Ser Phe Arg Gly Gly Met Gly Ser Gly Gly Leu Ala
50 55 60
Thr Gly Ile Ala Gly Gly Leu Ala Gly Met Gly Gly Ile Gln Asn Glu
65 70 75 80
Lys Glu Thr Met Gln Ser Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp
85 90 95
Arg Val Arg Ser Leu Glu Thr Glu Asn Arg Arg Leu Glu Ser Lys Ile
100 105 110
Arg Glu His Leu Glu Lys Lys Gly Pro Gln Val Arg Asp Trp Ser His
115 120 125
Tyr Phe Lys Ile Ile Glu Asp Leu Arg Ala Gln Ile Phe Ala Asn Thr
130 135 140
Val Asp Asn Ala Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu Ala
145 150 155 160
Ala Asp Asp Phe Arg Val Lys Tyr Glu Thr Glu Leu Ala Met Arg Gln
165 170 175
Ser Val Glu Asn Asp Ile His Gly Leu Arg Lys Val Ile Asp Asp Thr
180 185 190
Asn Ile Thr Arg Leu Gln Leu Glu Thr Glu Ile Glu Ala Leu Lys Glu
195 200 205
Glu Leu Leu Phe Met Lys Lys Asn His Glu Glu Glu Val Lys Gly Leu
210 215 220
Gln Ala Gln Ile Ala Ser Ser Gly Leu Thr Val Glu Val Asp Ala Pro

225	230	235	240
Lys Ser Gln Asp Leu Ala Lys Ile Met Ala Asp Ile Arg Ala Gln Tyr			
245	250	255	
Asp Glu Leu Ala Arg Lys Asn Arg Glu Glu Leu Asp Lys Tyr Trp Ser			
260	265	270	
Gln Gln Ile Glu Glu Ser Thr Thr Val Val Thr Thr Gln Ser Ala Glu			
275	280	285	
Val Gly Ala Ala Glu Thr Thr Leu Thr Glu Leu Arg Arg Thr Val Gln			
290	295	300	
Ser Leu Glu Ile Asp Leu Asp Ser Met Arg Asn Leu Lys Ala Ser Leu			
305	310	315	320
Glu Asn Ser Leu Arg Glu Val Glu Ala Arg Tyr Ala Leu Gln Met Glu			
325	330	335	
Gln Leu Asn Gly Ile Leu Leu His Leu Glu Ser Glu Leu Ala Gln Thr			
340	345	350	
Arg Ala Glu Gly Gln Arg Gln Ala Gln Glu Tyr Glu Ala Leu Leu Asn			
355	360	365	
Ile Lys Val Lys Leu Glu Ala Glu Ile Ala Thr Tyr Arg Arg Leu Leu			
370	375	380	
Glu Asp Gly Glu Asp Phe Asn Leu Gly Asp Ala Leu Asp Ser Ser Asn			
385	390	395	400
Ser Met Gln Thr Ile Gln Lys Thr Thr Thr Arg Arg Ile Val Asp Gly			
405	410	415	
Lys Val Val Ser Glu Thr Asn Asp Thr Lys Val Leu Arg His			
420	425	430	

<221> CDS

1241.22

<222> (171)..(968)

<400> 91

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ttctttgaag gagatgctaa gtttggggaa agaaacgaag ggagcggaca aggaggagaa 120
ggtgcctgaa tgggaacccc ccgaagcgcc tgaaaaggag agacaggagg atg atg 176

Met Met

1

tcc cag ctg gag ctg ctg agt ggg gga gag atg ctg tgc ggt ggc ttc 224
Ser Gln Leu Glu Leu Leu Ser Gly Gly Glu Met Leu Cys Gly Gly Phe

5

10

15

tac cct cgg ctg tcc tgc tgc ctg cgg agt gac agc ccg ggg cta ggg 272
Tyr Pro Arg Leu Ser Cys Cys Leu Arg Ser Asp Ser Pro Gly Leu Gly

20

25

30

cgc ctg gag aat aag ata ttt tct gtt acc aac aac aca gaa tgt ggg 320
Arg Leu Glu Asn Lys Ile Phe Ser Val Thr Asn Asn Thr Glu Cys Gly

35

40

45

50

aag tta ctg gag gaa atc aaa tgt gca ctt tgc tct cca cat tct caa 368
Lys Leu Leu Glu Glu Ile Lys Cys Ala Leu Cys Ser Pro His Ser Gln

55

60

65

agc ctg ttc cac tca cct gag aga gaa gtc ttg gaa aga gac cta gta 416
Ser Leu Phe His Ser Pro Glu Arg Glu Val Leu Glu Arg Asp Leu Val

70

75

80

ctt cct ctg ctc tgc aaa gac tat tgc aaa gaa ttc ttt tac act tgc 464
Leu Pro Leu Leu Cys Lys Asp Tyr Cys Lys Glu Phe Phe Tyr Thr Cys

85

90

95

cga ggc cat att cca ggt ttc ctt caa aca act gcg gat gag ttt tgc 512
Arg Gly His Ile Pro Gly Phe Leu Gln Thr Thr Ala Asp Glu Phe Cys

100

105

110

ttt tac tat gca aga aaa gat ggt ggg ttg tgc ttt cca gat ttt cca 560
Phe Tyr Tyr Ala Arg Lys Asp Gly Gly Leu Cys Phe Pro Asp Phe Pro

115

120

125

130

1241.22

aga aaa caa gtc aga gga cca gca tct aac tac ttg gac cag atg gaa	608
Arg Lys Gln Val Arg Gly Pro Ala Ser Asn Tyr Leu Asp Gln Met Glu	
135 140 145	
gaa tat gac aaa gtg gaa gag atc agc aga aag cac aaa cac aac tgc	656
Glu Tyr Asp Lys Val Glu Glu Ile Ser Arg Lys His Lys His Asn Cys	
150 155 160	
ttc tgt att cag gag gtt gtg agt ggg ctg cgg cag ccc gtt ggt gcc	704
Phe Cys Ile Gln Glu Val Val Ser Gly Leu Arg Gln Pro Val Gly Ala	
165 170 175	
ctg cat agt ggg gat ggc tcg caa cgt ctc ttc att ctg gaa aaa gaa	752
Leu His Ser Gly Asp Gly Ser Gln Arg Leu Phe Ile Leu Glu Lys Glu	
180 185 190	
ggc tat gtg aag ata ctt acc cct gaa gga gaa att ttc aag gag cct	800
Gly Tyr Val Lys Ile Leu Thr Pro Glu Gly Glu Ile Phe Lys Glu Pro	
195 200 205 210	
tat ttg gac att cac aaa ctt gtt caa agt gga ata aag gtt ggc ttt	848
Tyr Leu Asp Ile His Lys Leu Val Gln Ser Gly Ile Lys Val Gly Phe	
215 220 225	
tta aat ttt att tat ttt tgt gct ggc tac gtt aat ttt att tta gtg	896
Leu Asn Phe Ile Tyr Phe Cys Ala Gly Tyr Val Asn Phe Ile Leu Val	
230 235 240	
tta cct tcc tca ctg aag gta ttt ctt tgt aat aaa aga aag aat ctt	944
Leu Pro Ser Ser Leu Lys Val Phe Leu Cys Asn Lys Arg Lys Asn Leu	
245 250 255	
gca gga gaa aat aag ggg gca aca taagaaacaa taattatggc acctgaatta	998
Ala Gly Glu Asn Lys Gly Ala Thr	
260 265	
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<210> 92

<211> 266

<212> PRT

1241.22

<213> Homo sapiens

<400> 92

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Gly Phe Tyr Pro Arg Leu Ser Cys Cys Leu Arg Ser Asp Ser Pro Gly
             20             25             30
Leu Gly Arg Leu Glu Asn Lys Ile Phe Ser Val Thr Asn Asn Thr Glu
             35             40             45
Cys Gly Lys Leu Leu Glu Glu Ile Lys Cys Ala Leu Cys Ser Pro His
             50             55             60
Ser Gln Ser Leu Phe His Ser Pro Glu Arg Glu Val Leu Glu Arg Asp
  65             70             75             80
Leu Val Leu Pro Leu Leu Cys Lys Asp Tyr Cys Lys Glu Phe Phe Tyr
             85             90             95
Thr Cys Arg Gly His Ile Pro Gly Phe Leu Gln Thr Thr Ala Asp Glu
             100            105            110
Phe Cys Phe Tyr Tyr Ala Arg Lys Asp Gly Gly Leu Cys Phe Pro Asp
             115            120            125
Phe Pro Arg Lys Gln Val Arg Gly Pro Ala Ser Asn Tyr Leu Asp Gln
             130            135            140
Met Glu Glu Tyr Asp Lys Val Glu Glu Ile Ser Arg Lys His Lys His
  145            150            155            160
Asn Cys Phe Cys Ile Gln Glu Val Val Ser Gly Leu Arg Gln Pro Val
             165            170            175
Gly Ala Leu His Ser Gly Asp Gly Ser Gln Arg Leu Phe Ile Leu Glu
             180            185            190
Lys Glu Gly Tyr Val Lys Ile Leu Thr Pro Glu Gly Glu Ile Phe Lys
             195            200            205
Glu Pro Tyr Leu Asp Ile His Lys Leu Val Gln Ser Gly Ile Lys Val
             210            215            220
Gly Phe Leu Asn Phe Ile Tyr Phe Cys Ala Gly Tyr Val Asn Phe Ile
  225            230            235            240

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1241.22

Leu Val Leu Pro Ser Ser Leu Lys Val Phe Leu Cys Asn Lys Arg Lys

245

250

255

Asn Leu Ala Gly Glu Asn Lys Gly Ala Thr

260

265

<210> 93

<211> 1639

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (75)..(371)

<400> 93

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Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala

1

5

10

ttc ctg att tct gca gct ctg tgt gaa ggt gca gtt ttg cca agg agt 158

Phe Leu Ile Ser Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser

15

20

25

gct aaa gaa ctt aga tgt cag tgc ata aag aca tac tcc aaa cct ttc 206

Ala Lys Glu Leu Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe

30

35

40

cac ccc aaa ttt atc aaa gaa ctg aga gtg att gag agt gga cca cac 254

His Pro Lys Phe Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His

45

50

55

60

tgc gcc aac aca gaa att att gta aag ctt tct gat gga aga gag ctc 302

Cys Ala Asn Thr Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu

65

70

75

tgt ctg gac ccc aag gaa aac tgg gtg cag agg gtt gtg gag aag ttt 350

Cys Leu Asp Pro Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe

80

85

90

1241.22

ttg aag agg gct gag aat tca taaaaaatt cattctctgt ggtatccaag 401

Leu Lys Arg Ala Glu Asn Ser

95

aatcagtga gatgccagt aaacttcaag caaatctact tcaacacttc atgtattgtg 461
tgggtctgtt gtagggttgc cagatgcaat acaagattcc tggttaaatt tgaatttcag 521
taaacaatga atagtttttc attgtaccat gaaatatcca gaacatactt atagttaaag 581
tattatttat ttgaatctac aaaaaacaac aaataatttt taaatataag gattttccta 641
gatattgcac gggagaatat acaaatagca aaattgagcc aagggcccaag agaatatccg 701
aactttaatt tcaggaattg aatgggtttg ctagaatgtg atatttgaag catcacataa 761
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gtaaatttat tttatttttag atattaaatg atgttttatt agataaattt caatcagggg 1181
ttttagatta aacaaagaaa caattgggta cccagttaaa ttttcatttc agataaaca 1241
caaataattt tttagtataa gtacattatt gtttatctga aagttttaat tgaactaaca 1301
atcctagttt gatactccca gtcttgtcat tgccagctgt gttggtagtg ctgtgttgaa 1361
ttacggaata atgagttaga actattaaaa cagccaaaac tccacagtca atattagtaa 1421
tttcttgctg gttgaaactt gtttattatg tacaataga ttcttataat attattttaaa 1481
tgactgcatt tttaaataca aggctttata tttttaactt taagatgttt ttatgtgctc 1541
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aaaatataat ttgttgtcaa agtaaaaaaa aaaaaaaa 1639

<210> 94

<211> 99

<212> PRT

<213> Homo sapiens

<400> 94

Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala Phe Leu Ile Ser

1

5

10

15

1241.22

Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser Ala Lys Glu Leu
20 25 30
Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe
35 40 45
Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr
50 55 60
Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro
65 70 75 80
Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe Leu Lys Arg Ala
85 90 95
Glu Asn Ser

<210> 95

<211> 3293

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (8)..(1945)

<400> 95

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1 5 10
tgc tgc tgc tgt cct cgc gtc gcg ggt gtg ccc gga gag gct gag cag 97
Cys Cys Cys Cys Pro Arg Val Ala Gly Val Pro Gly Glu Ala Glu Gln
15 20 25 30
cct gcg cct gag ctg gtg gag gtg gaa gtg ggc agc aca gcc ctt ctg 145
Pro Ala Pro Glu Leu Val Glu Val Glu Val Gly Ser Thr Ala Leu Leu
35 40 45
aag tgc ggc ctc tcc cag tcc caa ggc aac ctc agc cat gtc gac tgg 193
Lys Cys Gly Leu Ser Gln Ser Gln Gly Asn Leu Ser His Val Asp Trp
50 55 60

1241.22

ttt tct gtc cac aag gag aag cgg acg ctc atc ttc cgt gtg cgc cag	241
Phe Ser Val His Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln	
65 70 75	
ggc cag ggc cag agc gaa cct ggg gag tac gag cag cgg ctc agc ctc	289
Gly Gln Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu	
80 85 90	
cag gac aga ggg gct act ctg gcc ctg act caa gtc acc ccc caa gac	337
Gln Asp Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp	
95 100 105 110	
gag cgc atc ttc ttg tgc cag ggc aag cgc cct cgg tcc cag gag tac	385
Glu Arg Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr	
115 120 125	
cgc atc cag ctc cgc gtc tac aaa gct ccg gag gag cca aac atc cag	433
Arg Ile Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln	
130 135 140	
gtc aac ccc ctg ggc atc cct gtg aac agt aag gag cct gag gag gtc	481
Val Asn Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val	
145 150 155	
gct acc tgt gta ggg agg aac ggg tac ccc att cct caa gtc atc tgg	529
Ala Thr Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp	
160 165 170	
tac aag aat ggc cgg cct ctg aag gag gag aag aac cgg gtc cac att	577
Tyr Lys Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn Arg Val His Ile	
175 180 185 190	
cag tcg tcc cag act gtg gag tcg agt ggt ttg tac acc ttg cag agt	625
Gln Ser Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser	
195 200 205	
att ctg aag gca cag ctg gtt aaa gaa gac aaa gat gcc cag ttt tac	673
Ile Leu Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr	
210 215 220	
tgt gag ctc aac tac cgg ctg ccc agt ggg aac cac atg aag gag tcc	721

1241.22

Cys Glu Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser	
225 230 235	
agg gaa gtc acc gtc cct gtt ttc tac ccg aca gaa aaa gtg tgg ctg	769
Arg Glu Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu	
240 245 250	
gaa gtg gag ccc gtg gga atg ctg aag gaa ggg gac cgc gtg gaa atc	817
Glu Val Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile	
255 260 265 270	
agg tgt ttg gct gat ggc aac cct cca cca cac ttc agc atc agc aag	865
Arg Cys Leu Ala Asp Gly Asn Pro Pro Pro His Phe Ser Ile Ser Lys	
275 280 285	
cag aac ccc agc acc agg gag gca gag gaa gag aca acc aac gac aac	913
Gln Asn Pro Ser Thr Arg Glu Ala Glu Glu Glu Thr Thr Asn Asp Asn	
290 295 300	
ggg gtc ctg gtg ctg gag cct gcc cgg aag gaa cac agt ggg cgc tat	961
Gly Val Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr	
305 310 315	
gaa tgt cag gcc tgg aac ttg gac acc atg ata tcg ctg ctg agt gaa	1009
Glu Cys Gln Ala Trp Asn Leu Asp Thr Met Ile Ser Leu Leu Ser Glu	
320 325 330	
cca cag gaa cta ctg gtg aac tat gtg tct gac gtc cga gtg agt ccc	1057
Pro Gln Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro	
335 340 345 350	
gca gcc cct gag aga cag gaa ggc agc agc ctc acc ctg acc tgt gag	1105
Ala Ala Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu	
355 360 365	
gca gag agt agc cag gac ctc gag ttc cag tgg ctg aga gaa gag aca	1153
Ala Glu Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr	
370 375 380	
gac cag gtg ctg gaa agg ggg cct gtg ctt cag ttg cat gac ctg aaa	1201
Asp Gln Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys	
385 390 395	

1241.22

cgg gag gca gga ggc ggc tat cgc tgc gtg gcg tct gtg ccc agc ata	1249
Arg Glu Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile	
400 405 410	
ccc ggc ctg aac cgc aca cag ctg gtc aag ctg gcc att ttt ggc ccc	1297
Pro Gly Leu Asn Arg Thr Gln Leu Val Lys Leu Ala Ile Phe Gly Pro	
415 420 425 430	
cct tgg atg gca ttc aag gag agg aag gtg tgg gtg aaa gag aat atg	1345
Pro Trp Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met	
435 440 445	
gtg ttg aat ctg tct tgt gaa gcg tca ggg cac ccc cgg ccc acc atc	1393
Val Leu Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile	
450 455 460	
tcc tgg aac gtc aac ggc acg gca agt gaa caa gac caa gat cca cag	1441
Ser Trp Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln	
465 470 475	
cga gtc ctg agc acc ctg aat gtc ctc gtg acc ccg gag ctg ttg gag	1489
Arg Val Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu	
480 485 490	
aca ggt gtt gaa tgc acg gcc tcc aac gac ctg ggc aaa aac acc agc	1537
Thr Gly Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser	
495 500 505 510	
atc ctc ttc ctg gag ctg gtc aat tta acc acc ctc aca cca gac tcc	1585
Ile Leu Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser	
515 520 525	
aac aca acc act ggc ctc agc act tcc act gcc agt cct cat acc aga	1633
Asn Thr Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg	
530 535 540	
gcc aac agc acc tcc aca gag aga aag ctg ccg gag ccg gag agc cgg	1681
Ala Asn Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg	
545 550 555	
ggc gtg gtc atc gtg gct gtg att gtg tgc atc ctg gtc ctg gcg gtg	1729

1241.22

Gly Val Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val

560 565 570

ctg ggc gct gtc ctc tat ttc ctc tat aag aag ggc aag ctg ccg tgc 1777

Leu Gly Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys

575 580 585 590

agg cgc tca ggg aag cag gag atc acg ctg ccc ccg tct cgt aag acc 1825

Arg Arg Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Thr

595 600 605

gaa ctt gta gtt gaa gtt aag tca gat aag ctc cca gaa gag atg ggc 1873

Glu Leu Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly

610 615 620

ctc ctg cag ggc agc agc ggt gac aag agg gct ccg gga gac cag gga 1921

Leu Leu Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly

625 630 635

gag aaa tac atc gat ctg agg cat tagccccgaa tcacttcagc tcccttcctt 1975

Glu Lys Tyr Ile Asp Leu Arg His

640 645

gcctggacca ttcccagctc cctgctcact cttctctcag ccaaagctca aagggactag 2035

agagaagcct cctgctcccc tcgctgcac accccctttc agagggccac tgggttagga 2095

cctgaggacc tcacttgccc ctgcaaggcc cgcttttcag ggaccagtcc accaccatct 2155

cctccacgtt gagtgaagct catcccaagc aaggagcccc agtctcccga gcgggtagga 2215

gagtttcttg cagaacgtgt tttttcttta cacacattat gctgtaaata cgctcgtcct 2275

gccagcagct gagctgggta gcctctctga gctggtttcc tgccccaag gctggcattc 2335

caccatccag gtgcaccact gaagtgagga cacaccggag ccaggcgctt gctcatgttg 2395

aagtgcgctg ttcacacccg ctccggagag caccacagca gcatccagaa gcagctgcag 2455

tgcaagcttg catgcctgcg tgttgctgca ccaccctcct gtctgcctct tcaaagtctc 2515

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cacaaagtca gacgagacca tcctggctaa cacggtgaaa ccctgtctct actaaaaata 2695

caaaaaaaaa ttagctaggc gtagtggttg gcacctatag tcccagctac tcggaaggct 2755

gaagcaggag aatggtatga atccaggagg tggagcttgc agtgagccga gaccgtgcc 2815

ctgcactcca gcctgggcaa cacagcgaga ctccgtctcg aggaaaaaaaaa aaatcgtgct 2875

1241.22

cgtagcagct ggctctgttt cgagtcaggt gaattagcct caatccccgt gttcacttgc 2935
tcccatagcc ctcttgatgg atcacgtaaa actgaaaggc agcggggagc agacaaagat 2995
gaggtctaca ctgtccttca tggggattaa agctatgggt atattagcac caaacttcta 3055
caaaccaagc tcaggaccca accctagaag ggcccaaagt agagaatggt acttagggat 3115
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gtgtgtatat atggttttgt caggtgtgta aatttgcaaa ttgtttcctt tatatatgta 3235
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<210> 96

<211> 646

<212> PRT

<213> Homo sapiens

<400> 96

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Cys Cys Pro Arg Val Ala Gly Val Pro Gly Glu Ala Glu Gln Pro Ala
20 25 30
Pro Glu Leu Val Glu Val Glu Val Gly Ser Thr Ala Leu Leu Lys Cys
35 40 45
Gly Leu Ser Gln Ser Gln Gly Asn Leu Ser His Val Asp Trp Phe Ser
50 55 60
Val His Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln Gly Gln
65 70 75 80
Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu Gln Asp
85 90 95
Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp Glu Arg
100 105 110
Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr Arg Ile
115 120 125
Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln Val Asn
130 135 140
Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val Ala Thr

1241.22

145	150	155	160
Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp Tyr Lys			
165	170	175	
Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn Arg Val His Ile Gln Ser			
180	185	190	
Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser Ile Leu			
195	200	205	
Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr Cys Glu			
210	215	220	
Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser Arg Glu			
225	230	235	240
Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu Glu Val			
245	250	255	
Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile Arg Cys			
260	265	270	
Leu Ala Asp Gly Asn Pro Pro Pro His Phe Ser Ile Ser Lys Gln Asn			
275	280	285	
Pro Ser Thr Arg Glu Ala Glu Glu Glu Thr Thr Asn Asp Asn Gly Val			
290	295	300	
Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr Glu Cys			
305	310	315	320
Gln Ala Trp Asn Leu Asp Thr Met Ile Ser Leu Leu Ser Glu Pro Gln			
325	330	335	
Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro Ala Ala			
340	345	350	
Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu Ala Glu			
355	360	365	
Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr Asp Gln			
370	375	380	
Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys Arg Glu			
385	390	395	400

1241.22

Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile Pro Gly
405 410 415

Leu Asn Arg Thr Gln Leu Val Lys Leu Ala Ile Phe Gly Pro Pro Trp
420 425 430

Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met Val Leu
435 440 445

Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile Ser Trp
450 455 460

Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln Arg Val
465 470 475 480

Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu Thr Gly
485 490 495

Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser Ile Leu
500 505 510

Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser Asn Thr
515 520 525

Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg Ala Asn
530 535 540

Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg Gly Val
545 550 555 560

Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val Leu Gly
565 570 575

Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys Arg Arg
580 585 590

Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Thr Glu Leu
595 600 605

Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly Leu Leu
610 615 620

Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly Glu Lys
625 630 635 640

Tyr Ile Asp Leu Arg His
645

<210> 97

<211> 1642

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (158)..(1279)

<400> 97

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 ctgacttttg aaatctcggt taaccttcaa actggcg atg tca agg gtt cca agt 175

Met Ser Arg Val Pro Ser

1

5

cct cca cct ccg gca gaa atg tcg agt ggc ccc gta gct gag agt tgg 223

Pro Pro Pro Pro Ala Glu Met Ser Ser Gly Pro Val Ala Glu Ser Trp

10

15

20

tgc tac aca cag atc aag gta gtg aaa ttc tcc tac atg tgg acc atc 271

Cys Tyr Thr Gln Ile Lys Val Val Lys Phe Ser Tyr Met Trp Thr Ile

25

30

35

aat aac ttt agc ttt tgc cgg gag gaa atg ggt gaa gtc att aaa agt 319

Asn Asn Phe Ser Phe Cys Arg Glu Glu Met Gly Glu Val Ile Lys Ser

40

45

50

tct aca ttt tca tca gga gca aat gat aaa ctg aaa tgg tgt ttg cga 367

Ser Thr Phe Ser Ser Gly Ala Asn Asp Lys Leu Lys Trp Cys Leu Arg

55

60

65

70

gta aac ccc aaa ggg tta gat gaa gaa agc aaa gat tac ctg tca ctt 415

Val Asn Pro Lys Gly Leu Asp Glu Glu Ser Lys Asp Tyr Leu Ser Leu

75

80

85

tac ctg tta ctg gtc agc tgt cca aag agt gaa gtt cgg gca aaa ttc 463

Tyr Leu Leu Leu Val Ser Cys Pro Lys Ser Glu Val Arg Ala Lys Phe

90

95

100

1241.22

aaa ttc tcc atc ctg aat gcc aag gga gaa gaa acc aaa gct atg gag	511
Lys Phe Ser Ile Leu Asn Ala Lys Gly Glu Glu Thr Lys Ala Met Glu	
105 110 115	
agt caa cgg gca tat agg ttt gtg caa ggc aaa gac tgg gga ttc aag	559
Ser Gln Arg Ala Tyr Arg Phe Val Gln Gly Lys Asp Trp Gly Phe Lys	
120 125 130	
aaa ttc atc cgt aga gat ttt ctt ttg gat gag gcc aac ggg ctt ctc	607
Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp Glu Ala Asn Gly Leu Leu	
135 140 145 150	
cct gat gac aag ctt acc ctc ttc tgc gag gtg agt gtt gtg caa gat	655
Pro Asp Asp Lys Leu Thr Leu Phe Cys Glu Val Ser Val Val Gln Asp	
155 160 165	
tct gtc aac att tct ggc cag aat acc atg aac atg gta aag gtt cct	703
Ser Val Asn Ile Ser Gly Gln Asn Thr Met Asn Met Val Lys Val Pro	
170 175 180	
gag tgc cgg ctg gca gat gag tta gga gga ctg tgg gag aat tcc cgg	751
Glu Cys Arg Leu Ala Asp Glu Leu Gly Gly Leu Trp Glu Asn Ser Arg	
185 190 195	
ttc aca gac tgc tgc ttg tgt gtt gcc ggc cag gaa ttc cag gct cac	799
Phe Thr Asp Cys Cys Leu Cys Val Ala Gly Gln Glu Phe Gln Ala His	
200 205 210	
aag gct atc tta gca gct cgt tct ccg gtt ttt agt gcc atg ttt gaa	847
Lys Ala Ile Leu Ala Ala Arg Ser Pro Val Phe Ser Ala Met Phe Glu	
215 220 225 230	
cat gaa atg gag gag agc aaa aag aat cga gtt gaa atc aat gat gtg	895
His Glu Met Glu Glu Ser Lys Lys Asn Arg Val Glu Ile Asn Asp Val	
235 240 245	
gag cct gaa gtt ttt aag gaa atg atg tgc ttc att tac acg ggg aag	943
Glu Pro Glu Val Phe Lys Glu Met Met Cys Phe Ile Tyr Thr Gly Lys	
250 255 260	
gct cca aac ctc gac aaa atg gct gat gat ttg ctg gca gct gct gac	991

1241.22

Ala Pro Asn Leu Asp Lys Met Ala Asp Asp Leu Leu Ala Ala Ala Asp
265 270 275

aag tat gcc ctg gag cgc tta aag gtc atg tgt gag gat gcc ctc tgc 1039
Lys Tyr Ala Leu Glu Arg Leu Lys Val Met Cys Glu Asp Ala Leu Cys
280 285 290

agt aac ctg tcc gtg gag aac gct gca gaa att ctc atc ctg gcc gac 1087
Ser Asn Leu Ser Val Glu Asn Ala Ala Glu Ile Leu Ile Leu Ala Asp
295 300 305 310

ctc cac agt gca gat cag ttg aaa act cag gca gtg gat ttc atc aac 1135
Leu His Ser Ala Asp Gln Leu Lys Thr Gln Ala Val Asp Phe Ile Asn
315 320 325

tat cat gct tcg gat gtc ttg gag acc tct ggg tgg aag tca atg gtg 1183
Tyr His Ala Ser Asp Val Leu Glu Thr Ser Gly Trp Lys Ser Met Val
330 335 340

gtg tca cat ccc cac ttg gtg gct gag gca tac cgc tct ctg gct tca 1231
Val Ser His Pro His Leu Val Ala Glu Ala Tyr Arg Ser Leu Ala Ser
345 350 355

gca cag tgc cct ttt ctg gga ccc cca cgc aaa cgc ctg aag caa tcc 1279
Ala Gln Cys Pro Phe Leu Gly Pro Pro Arg Lys Arg Leu Lys Gln Ser
360 365 370

taagatcctg cttgttgtaa gactccgttt aatttccaga agcagcagcc actgttgctg 1339
ccactgacca ccaggtagac agcgcaatct gtggagcttt tactctgttg tgaggggaag 1399
agactgcatt gtggccccag acttttaaaa cagcactaaa taacttgggg gaaacggggg 1459
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gtttgatact gtggggattc agtttaggcg ctggcccag gatatcccag cggttgttact 1579
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agg 1642

<210> 98

<211> 374

<212> PRT

<213> Homo sapiens

1241.22

<400> 98

Met	Ser	Arg	Val	Pro	Ser	Pro	Pro	Pro	Pro	Ala	Glu	Met	Ser	Ser	Gly
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Pro	Val	Ala	Glu	Ser	Trp	Cys	Tyr	Thr	Gln	Ile	Lys	Val	Val	Lys	Phe
			20					25					30		
Ser	Tyr	Met	Trp	Thr	Ile	Asn	Asn	Phe	Ser	Phe	Cys	Arg	Glu	Glu	Met
		35					40					45			
Gly	Glu	Val	Ile	Lys	Ser	Ser	Thr	Phe	Ser	Ser	Gly	Ala	Asn	Asp	Lys
	50					55					60				
Leu	Lys	Trp	Cys	Leu	Arg	Val	Asn	Pro	Lys	Gly	Leu	Asp	Glu	Glu	Ser
65					70					75					80
Lys	Asp	Tyr	Leu	Ser	Leu	Tyr	Leu	Leu	Leu	Val	Ser	Cys	Pro	Lys	Ser
				85					90					95	
Glu	Val	Arg	Ala	Lys	Phe	Lys	Phe	Ser	Ile	Leu	Asn	Ala	Lys	Gly	Glu
		100						105					110		
Glu	Thr	Lys	Ala	Met	Glu	Ser	Gln	Arg	Ala	Tyr	Arg	Phe	Val	Gln	Gly
		115					120					125			
Lys	Asp	Trp	Gly	Phe	Lys	Lys	Phe	Ile	Arg	Arg	Asp	Phe	Leu	Leu	Asp
	130					135					140				
Glu	Ala	Asn	Gly	Leu	Leu	Pro	Asp	Asp	Lys	Leu	Thr	Leu	Phe	Cys	Glu
145					150					155					160
Val	Ser	Val	Val	Gln	Asp	Ser	Val	Asn	Ile	Ser	Gly	Gln	Asn	Thr	Met
				165					170					175	
Asn	Met	Val	Lys	Val	Pro	Glu	Cys	Arg	Leu	Ala	Asp	Glu	Leu	Gly	Gly
		180						185					190		
Leu	Trp	Glu	Asn	Ser	Arg	Phe	Thr	Asp	Cys	Cys	Leu	Cys	Val	Ala	Gly
		195					200					205			
Gln	Glu	Phe	Gln	Ala	His	Lys	Ala	Ile	Leu	Ala	Ala	Arg	Ser	Pro	Val
	210					215					220				
Phe	Ser	Ala	Met	Phe	Glu	His	Glu	Met	Glu	Glu	Ser	Lys	Lys	Asn	Arg
225					230					235					240
Val	Glu	Ile	Asn	Asp	Val	Glu	Pro	Glu	Val	Phe	Lys	Glu	Met	Met	Cys

1241.22

245 250 255
Phe Ile Tyr Thr Gly Lys Ala Pro Asn Leu Asp Lys Met Ala Asp Asp
260 265 270
Leu Leu Ala Ala Ala Asp Lys Tyr Ala Leu Glu Arg Leu Lys Val Met
275 280 285
Cys Glu Asp Ala Leu Cys Ser Asn Leu Ser Val Glu Asn Ala Ala Glu
290 295 300
Ile Leu Ile Leu Ala Asp Leu His Ser Ala Asp Gln Leu Lys Thr Gln
305 310 315 320
Ala Val Asp Phe Ile Asn Tyr His Ala Ser Asp Val Leu Glu Thr Ser
325 330 335
Gly Trp Lys Ser Met Val Val Ser His Pro His Leu Val Ala Glu Ala
340 345 350
Tyr Arg Ser Leu Ala Ser Ala Gln Cys Pro Phe Leu Gly Pro Pro Arg
355 360 365
Lys Arg Leu Lys Gln Ser
370

<210> 99

<211> 5722

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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Met Gly

1

ctg gcc tgg gga cta ggc gtc ctg ttc ctg atg cat gtg tgt ggc acc 165
Leu Ala Trp Gly Leu Gly Val Leu Phe Leu Met His Val Cys Gly Thr

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5	10	15	
aac cgc att cca gag tct ggc gga gac aac agc gtg ttt gac atc ttt	213		
Asn Arg Ile Pro Glu Ser Gly Gly Asp Asn Ser Val Phe Asp Ile Phe			
20	25	30	
gaa ctc acc ggg gcc gcc cgc aag ggg tct ggg cgc cga ctg gtg aag	261		
Glu Leu Thr Gly Ala Ala Arg Lys Gly Ser Gly Arg Arg Leu Val Lys			
35	40	45	50
ggc ccc gac cct tcc agc cca gct ttc cgc atc gag gat gcc aac ctg	309		
Gly Pro Asp Pro Ser Ser Pro Ala Phe Arg Ile Glu Asp Ala Asn Leu			
55	60	65	
atc ccc cct gtg cct gat gac aag ttc caa gac ctg gtg gat gct gtg	357		
Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp Ala Val			
70	75	80	
cgg gca gaa aag ggt ttc ctc ctt ctg gca tcc ctg agg cag atg aag	405		
Arg Ala Glu Lys Gly Phe Leu Leu Leu Ala Ser Leu Arg Gln Met Lys			
85	90	95	
aag acc cgg ggc acg ctg ctg gcc ctg gag cgg aaa gac cac tct ggc	453		
Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His Ser Gly			
100	105	110	
cag gtc ttc agc gtg gtg tcc aat ggc aag gcg ggc acc ctg gac ctc	501		
Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu Asp Leu			
115	120	125	130
agc ctg acc gtc caa gga aag cag cac gtg gtg tct gtg gaa gaa gct	549		
Ser Leu Thr Val Gln Gly Lys Gln His Val Val Ser Val Glu Glu Ala			
135	140	145	
ctc ctg gca acc ggc cag tgg aag agc atc acc ctg ttt gtg cag gaa	597		
Leu Leu Ala Thr Gly Gln Trp Lys Ser Ile Thr Leu Phe Val Gln Glu			
150	155	160	
gac agg gcc cag ctg tac atc gac tgt gaa aag atg gag aat gct gag	645		
Asp Arg Ala Gln Leu Tyr Ile Asp Cys Glu Lys Met Glu Asn Ala Glu			
165	170	175	

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ttg gac gtc ccc atc caa agc gtc ttc acc aga gac ctg gcc agc atc	693
Leu Asp Val Pro Ile Gln Ser Val Phe Thr Arg Asp Leu Ala Ser Ile	
180 185 190	
gcc aga ctc cgc atc gca aag ggg ggc gtc aat gac aat ttc cag ggg	741
Ala Arg Leu Arg Ile Ala Lys Gly Gly Val Asn Asp Asn Phe Gln Gly	
195 200 205 210	
gtg ctg cag aat gtg agg ttt gtc ttt gga acc aca cca gaa gac atc	789
Val Leu Gln Asn Val Arg Phe Val Phe Gly Thr Thr Pro Glu Asp Ile	
215 220 225	
ctc agg aac aaa ggc tgc tcc agc tct acc agt gtc ctc ctc acc ctt	837
Leu Arg Asn Lys Gly Cys Ser Ser Ser Thr Ser Val Leu Leu Thr Leu	
230 235 240	
gac aac aac gtg gtg aat ggt tcc agc cct gcc atc cgc act aac tac	885
Asp Asn Asn Val Val Asn Gly Ser Ser Pro Ala Ile Arg Thr Asn Tyr	
245 250 255	
att ggc cac aag aca aag gac ttg caa gcc atc tgc ggc atc tcc tgt	933
Ile Gly His Lys Thr Lys Asp Leu Gln Ala Ile Cys Gly Ile Ser Cys	
260 265 270	
gat gag ctg tcc agc atg gtc ctg gaa ctc agg ggc ctg cgc acc att	981
Asp Glu Leu Ser Ser Met Val Leu Glu Leu Arg Gly Leu Arg Thr Ile	
275 280 285 290	
gtg acc acg ctg cag gac agc atc cgc aaa gtg act gaa gag aac aaa	1029
Val Thr Thr Leu Gln Asp Ser Ile Arg Lys Val Thr Glu Glu Asn Lys	
295 300 305	
gag ttg gcc aat gag ctg agg cgg cct ccc cta tgc tat cac aac gga	1077
Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr His Asn Gly	
310 315 320	
gtt cag tac aga aat aac gag gaa tgg act gtt gat agc tgc act gag	1125
Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser Cys Thr Glu	
325 330 335	
tgt cac tgt cag aac tca gtt acc atc tgc aaa aag gtg tcc tgc ccc	1173
Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys Lys Val Ser Cys Pro	

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340	345	350	
atc atg ccc tgc tcc aat gcc aca gtt cct gat gga gaa tgc tgt cct	1221		
Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp Gly Glu Cys Cys Pro			
355	360	365	370
cgc tgt tgg ccc agc gac tct gcg gac gat ggc tgg tct cca tgg tcc	1269		
Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly Trp Ser Pro Trp Ser			
375	380	385	
gag tgg acc tcc tgt tct acg agc tgt ggc aat gga att cag cag cgc	1317		
Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn Gly Ile Gln Gln Arg			
390	395	400	
ggc cgc tcc tgc gat agc ctc aac aac cga tgt gag ggc tcc tcg gtc	1365		
Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys Glu Gly Ser Ser Val			
405	410	415	
cag aca cgg acc tgc cac att cag gag tgt gac aaa aga ttt aaa cag	1413		
Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp Lys Arg Phe Lys Gln			
420	425	430	
gat ggt ggc tgg agc cac tgg tcc ccg tgg tca tct tgt tct gtg aca	1461		
Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser Val Thr			
435	440	445	450
tgt ggt gat ggt gtg atc aca agg atc cgg ctc tgc aac tct ccc agc	1509		
Cys Gly Asp Gly Val Ile Thr Arg Ile Arg Leu Cys Asn Ser Pro Ser			
455	460	465	
ccc cag atg aat ggg aaa ccc tgt gaa ggc gaa gcg cgg gag acc aaa	1557		
Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala Arg Glu Thr Lys			
470	475	480	
gcc tgc aag aaa gac gcc tgc ccc atc aat gga ggc tgg ggt cct tgg	1605		
Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Gly Gly Trp Gly Pro Trp			
485	490	495	
tca cca tgg gac atc tgt tct gtc acc tgt gga gga ggg gta cag aaa	1653		
Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly Gly Gly Val Gln Lys			
500	505	510	

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cgt agt cgt ctc tgc aac aac ccc gca ccc cag ttt gga ggc aag gac	1701
Arg Ser Arg Leu Cys Asn Asn Pro Ala Pro Gln Phe Gly Gly Lys Asp	
515 520 525 530	
tgc gtt ggt gat gta aca gaa aac cag atc tgc aac aag cag gac tgt	1749
Cys Val Gly Asp Val Thr Glu Asn Gln Ile Cys Asn Lys Gln Asp Cys	
535 540 545	
cca att gat gga tgc ctg tcc aat ccc tgc ttt gcc ggc gtg aag tgt	1797
Pro Ile Asp Gly Cys Leu Ser Asn Pro Cys Phe Ala Gly Val Lys Cys	
550 555 560	
act agc tac cct gat ggc agc tgg aaa tgt ggt gct tgt ccc cct ggt	1845
Thr Ser Tyr Pro Asp Gly Ser Trp Lys Cys Gly Ala Cys Pro Pro Gly	
565 570 575	
tac agt gga aat ggc atc cag tgc aca gat gtt gat gag tgc aaa gaa	1893
Tyr Ser Gly Asn Gly Ile Gln Cys Thr Asp Val Asp Glu Cys Lys Glu	
580 585 590	
gtg cct gat gcc tgc ttc aac cac aat gga gag cac cgg tgt gag aac	1941
Val Pro Asp Ala Cys Phe Asn His Asn Gly Glu His Arg Cys Glu Asn	
595 600 605 610	
acg gac ccc ggc tac aac tgc ctg ccc tgc ccc cca cgc ttc acc ggc	1989
Thr Asp Pro Gly Tyr Asn Cys Leu Pro Cys Pro Pro Arg Phe Thr Gly	
615 620 625	
tca cag ccc ttc ggc cag ggt gtc gaa cat gcc acg gcc aac aaa cag	2037
Ser Gln Pro Phe Gly Gln Gly Val Glu His Ala Thr Ala Asn Lys Gln	
630 635 640	
gtg tgc aag ccc cgt aac ccc tgc acg gat ggg acc cac gac tgc aac	2085
Val Cys Lys Pro Arg Asn Pro Cys Thr Asp Gly Thr His Asp Cys Asn	
645 650 655	
aag aac gcc aag tgc aac tac ctg ggc cac tat agc gac ccc atg tac	2133
Lys Asn Ala Lys Cys Asn Tyr Leu Gly His Tyr Ser Asp Pro Met Tyr	
660 665 670	
cgc tgc gag tgc aag cct ggc tac gct ggc aat ggc atc atc tgc ggg	2181
Arg Cys Glu Cys Lys Pro Gly Tyr Ala Gly Asn Gly Ile Ile Cys Gly	

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675	680	685	690	
gag gac aca gac ctg gat ggc tgg ccc aat gag aac ctg gtg tgc gtg				2229
Glu Asp Thr Asp Leu Asp Gly Trp Pro Asn Glu Asn Leu Val Cys Val				
	695	700	705	
gcc aat gcg act tac cac tgc aaa aag gat aat tgc ccc aac ctt ccc				2277
Ala Asn Ala Thr Tyr His Cys Lys Lys Asp Asn Cys Pro Asn Leu Pro				
	710	715	720	
aac tca ggg cag gaa gac tat gac aag gat gga att ggt gat gcc tgt				2325
Asn Ser Gly Gln Glu Asp Tyr Asp Lys Asp Gly Ile Gly Asp Ala Cys				
	725	730	735	
gat gat gac gat gac aat gat aaa att cca gat gac agg gac aac tgt				2373
Asp Asp Asp Asp Asp Asn Asp Lys Ile Pro Asp Asp Arg Asp Asn Cys				
	740	745	750	
cca ttc cat tac aac cca gct cag tat gac tat gac aga gat gat gtg				2421
Pro Phe His Tyr Asn Pro Ala Gln Tyr Asp Tyr Asp Arg Asp Asp Val				
755	760	765	770	
gga gac cgc tgt gac aac tgt ccc tac aac cac aac cca gat cag gca				2469
Gly Asp Arg Cys Asp Asn Cys Pro Tyr Asn His Asn Pro Asp Gln Ala				
	775	780	785	
gac aca gac aac aat ggg gaa gga gac gcc tgt gct gca gac att gat				2517
Asp Thr Asp Asn Asn Gly Glu Gly Asp Ala Cys Ala Ala Asp Ile Asp				
	790	795	800	
gga gac ggt atc ctc aat gaa cgg gac aac tgc cag tac gtc tac aat				2565
Gly Asp Gly Ile Leu Asn Glu Arg Asp Asn Cys Gln Tyr Val Tyr Asn				
	805	810	815	
gtg gac cag aga gac act gat atg gat ggg gtt gga gat cag tgt gac				2613
Val Asp Gln Arg Asp Thr Asp Met Asp Gly Val Gly Asp Gln Cys Asp				
	820	825	830	
aat tgc ccc ttg gaa cac aat ccg gat cag ctg gac tct gac tca gac				2661
Asn Cys Pro Leu Glu His Asn Pro Asp Gln Leu Asp Ser Asp Ser Asp				
835	840	845	850	

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cgc att gga gat acc tgt gac aac aat cag gat att gat gaa gat ggc	2709
Arg Ile Gly Asp Thr Cys Asp Asn Asn Gln Asp Ile Asp Glu Asp Gly	
855 860 865	
cac cag aac aat ctg gac aac tgt ccc tat gtg ccc aat gcc aac cag	2757
His Gln Asn Asn Leu Asp Asn Cys Pro Tyr Val Pro Asn Ala Asn Gln	
870 875 880	
gct gac cat gac aaa gat ggc aag gga gat gcc tgt gac cac gat gat	2805
Ala Asp His Asp Lys Asp Gly Lys Gly Asp Ala Cys Asp His Asp Asp	
885 890 895	
gac aac gat ggc att cct gat gac aag gac aac tgc aga ctc gtg ccc	2853
Asp Asn Asp Gly Ile Pro Asp Asp Lys Asp Asn Cys Arg Leu Val Pro	
900 905 910	
aat ccc gac cag aag gac tct gac ggc gat ggt cga ggt gat gcc tgc	2901
Asn Pro Asp Gln Lys Asp Ser Asp Gly Asp Gly Arg Gly Asp Ala Cys	
915 920 925 930	
aaa gat gat ttt gac cat gac agt gtg cca gac atc gat gac atc tgt	2949
Lys Asp Asp Phe Asp His Asp Ser Val Pro Asp Ile Asp Asp Ile Cys	
935 940 945	
cct gag aat gtt gac atc agt gag acc gat ttc cgc cga ttc cag atg	2997
Pro Glu Asn Val Asp Ile Ser Glu Thr Asp Phe Arg Arg Phe Gln Met	
950 955 960	
att cct ctg gac ccc aaa ggg aca tcc caa aat gac cct aac tgg gtt	3045
Ile Pro Leu Asp Pro Lys Gly Thr Ser Gln Asn Asp Pro Asn Trp Val	
965 970 975	
gta cgc cat cag ggt aaa gaa ctc gtc cag act gtc aac tgt gat cct	3093
Val Arg His Gln Gly Lys Glu Leu Val Gln Thr Val Asn Cys Asp Pro	
980 985 990	
gga ctc gct gta ggt tat gat gag ttt aat gct gtg gac ttc agt ggc	3141
Gly Leu Ala Val Gly Tyr Asp Glu Phe Asn Ala Val Asp Phe Ser Gly	
995 1000 1005 1010	
acc ttc ttc atc aac acc gaa agg gac gat gac tat gct gga ttt gtc	3189
Thr Phe Phe Ile Asn Thr Glu Arg Asp Asp Asp Tyr Ala Gly Phe Val	

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1015	1020	1025	
ttt ggc tac cag tcc agc agc cgc ttt tat gtt gtg atg tgg aag caa			3237
Phe Gly Tyr Gln Ser Ser Ser Arg Phe Tyr Val Val Met Trp Lys Gln			
1030	1035	1040	
gtc acc cag tcc tac tgg gac acc aac ccc acg agg gct cag gga tac			3285
Val Thr Gln Ser Tyr Trp Asp Thr Asn Pro Thr Arg Ala Gln Gly Tyr			
1045	1050	1055	
tcg ggc ctt tct gtg aaa gtt gta aac tcc acc aca ggg cct ggc gag			3333
Ser Gly Leu Ser Val Lys Val Val Asn Ser Thr Thr Gly Pro Gly Glu			
1060	1065	1070	
cac ctg cgg aac gcc ctg tgg cac aca gga aac acc cct ggc cag gtg			3381
His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr Pro Gly Gln Val			
1075	1080	1085	1090
cgc acc ctg tgg cat gac cct cgt cac ata ggc tgg aaa gat ttc acc			3429
Arg Thr Leu Trp His Asp Pro Arg His Ile Gly Trp Lys Asp Phe Thr			
1095	1100	1105	
gcc tac aga tgg cgt ctc agc cac agg cca aag acg ggt ttc att aga			3477
Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe Ile Arg			
1110	1115	1120	
gtg gtg atg tat gaa ggg aag aaa atc atg gct gac tca gga ccc atc			3525
Val Val Met Tyr Glu Gly Lys Lys Ile Met Ala Asp Ser Gly Pro Ile			
1125	1130	1135	
tat gat aaa acc tat gct ggt ggt aga cta ggg ttg ttt gtc ttc tct			3573
Tyr Asp Lys Thr Tyr Ala Gly Gly Arg Leu Gly Leu Phe Val Phe Ser			
1140	1145	1150	
caa gaa atg gtg ttc ttc tct gac ctg aaa tac gaa tgt aga gat ccc			3621
Gln Glu Met Val Phe Phe Ser Asp Leu Lys Tyr Glu Cys Arg Asp Pro			
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5722

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<210> 100

<211> 1170

<212> PRT

<213> Homo sapiens

<400> 100

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20 25 30
Ile Phe Glu Leu Thr Gly Ala Ala Arg Lys Gly Ser Gly Arg Arg Leu
35 40 45
Val Lys Gly Pro Asp Pro Ser Ser Pro Ala Phe Arg Ile Glu Asp Ala
50 55 60
Asn Leu Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp
65 70 75 80
Ala Val Arg Ala Glu Lys Gly Phe Leu Leu Leu Ala Ser Leu Arg Gln
85 90 95
Met Lys Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His
100 105 110
Ser Gly Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu
115 120 125
Asp Leu Ser Leu Thr Val Gln Gly Lys Gln His Val Val Ser Val Glu
130 135 140
Glu Ala Leu Leu Ala Thr Gly Gln Trp Lys Ser Ile Thr Leu Phe Val
145 150 155 160
Gln Glu Asp Arg Ala Gln Leu Tyr Ile Asp Cys Glu Lys Met Glu Asn
165 170 175
Ala Glu Leu Asp Val Pro Ile Gln Ser Val Phe Thr Arg Asp Leu Ala
180 185 190
Ser Ile Ala Arg Leu Arg Ile Ala Lys Gly Gly Val Asn Asp Asn Phe

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195	200	205
Gln Gly Val Leu Gln Asn Val Arg Phe Val Phe Gly Thr Thr Pro Glu		
210	215	220
Asp Ile Leu Arg Asn Lys Gly Cys Ser Ser Ser Thr Ser Val Leu Leu		
225	230	235
Thr Leu Asp Asn Asn Val Val Asn Gly Ser Ser Pro Ala Ile Arg Thr		
245	250	255
Asn Tyr Ile Gly His Lys Thr Lys Asp Leu Gln Ala Ile Cys Gly Ile		
260	265	270
Ser Cys Asp Glu Leu Ser Ser Met Val Leu Glu Leu Arg Gly Leu Arg		
275	280	285
Thr Ile Val Thr Thr Leu Gln Asp Ser Ile Arg Lys Val Thr Glu Glu		
290	295	300
Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr His		
305	310	315
Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser Cys		
325	330	335
Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys Lys Val Ser		
340	345	350
Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp Gly Glu Cys		
355	360	365
Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly Trp Ser Pro		
370	375	380
Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn Gly Ile Gln		
385	390	395
Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys Glu Gly Ser		
405	410	415
Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp Lys Arg Phe		
420	425	430
Lys Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser		
435	440	445

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Val	Thr	Cys	Gly	Asp	Gly	Val	Ile	Thr	Arg	Ile	Arg	Leu	Cys	Asn	Ser
450						455						460			
Pro	Ser	Pro	Gln	Met	Asn	Gly	Lys	Pro	Cys	Glu	Gly	Glu	Ala	Arg	Glu
465					470					475				480	
Thr	Lys	Ala	Cys	Lys	Lys	Asp	Ala	Cys	Pro	Ile	Asn	Gly	Gly	Trp	Gly
				485					490					495	
Pro	Trp	Ser	Pro	Trp	Asp	Ile	Cys	Ser	Val	Thr	Cys	Gly	Gly	Gly	Val
			500					505					510		
Gln	Lys	Arg	Ser	Arg	Leu	Cys	Asn	Asn	Pro	Ala	Pro	Gln	Phe	Gly	Gly
	515						520						525		
Lys	Asp	Cys	Val	Gly	Asp	Val	Thr	Glu	Asn	Gln	Ile	Cys	Asn	Lys	Gln
	530					535					540				
Asp	Cys	Pro	Ile	Asp	Gly	Cys	Leu	Ser	Asn	Pro	Cys	Phe	Ala	Gly	Val
545					550					555				560	
Lys	Cys	Thr	Ser	Tyr	Pro	Asp	Gly	Ser	Trp	Lys	Cys	Gly	Ala	Cys	Pro
				565					570					575	
Pro	Gly	Tyr	Ser	Gly	Asn	Gly	Ile	Gln	Cys	Thr	Asp	Val	Asp	Glu	Cys
			580					585						590	
Lys	Glu	Val	Pro	Asp	Ala	Cys	Phe	Asn	His	Asn	Gly	Glu	His	Arg	Cys
		595					600							605	
Glu	Asn	Thr	Asp	Pro	Gly	Tyr	Asn	Cys	Leu	Pro	Cys	Pro	Pro	Arg	Phe
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Thr	Gly	Ser	Gln	Pro	Phe	Gly	Gln	Gly	Val	Glu	His	Ala	Thr	Ala	Asn
625					630					635				640	
Lys	Gln	Val	Cys	Lys	Pro	Arg	Asn	Pro	Cys	Thr	Asp	Gly	Thr	His	Asp
				645					650					655	
Cys	Asn	Lys	Asn	Ala	Lys	Cys	Asn	Tyr	Leu	Gly	His	Tyr	Ser	Asp	Pro
			660					665						670	
Met	Tyr	Arg	Cys	Glu	Cys	Lys	Pro	Gly	Tyr	Ala	Gly	Asn	Gly	Ile	Ile
	675							680						685	
Cys	Gly	Glu	Asp	Thr	Asp	Leu	Asp	Gly	Trp	Pro	Asn	Glu	Asn	Leu	Val
690						695						700			

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Cys Val Ala Asn Ala Thr Tyr His Cys Lys Lys Asp Asn Cys Pro Asn
705 710 715 720
Leu Pro Asn Ser Gly Gln Glu Asp Tyr Asp Lys Asp Gly Ile Gly Asp
725 730 735
Ala Cys Asp Asp Asp Asp Asp Asn Asp Lys Ile Pro Asp Asp Arg Asp
740 745 750
Asn Cys Pro Phe His Tyr Asn Pro Ala Gln Tyr Asp Tyr Asp Arg Asp
755 760 765
Asp Val Gly Asp Arg Cys Asp Asn Cys Pro Tyr Asn His Asn Pro Asp
770 775 780
Gln Ala Asp Thr Asp Asn Asn Gly Glu Gly Asp Ala Cys Ala Ala Asp
785 790 795 800
Ile Asp Gly Asp Gly Ile Leu Asn Glu Arg Asp Asn Cys Gln Tyr Val
805 810 815
Tyr Asn Val Asp Gln Arg Asp Thr Asp Met Asp Gly Val Gly Asp Gln
820 825 830
Cys Asp Asn Cys Pro Leu Glu His Asn Pro Asp Gln Leu Asp Ser Asp
835 840 845
Ser Asp Arg Ile Gly Asp Thr Cys Asp Asn Asn Gln Asp Ile Asp Glu
850 855 860
Asp Gly His Gln Asn Asn Leu Asp Asn Cys Pro Tyr Val Pro Asn Ala
865 870 875 880
Asn Gln Ala Asp His Asp Lys Asp Gly Lys Gly Asp Ala Cys Asp His
885 890 895
Asp Asp Asp Asn Asp Gly Ile Pro Asp Asp Lys Asp Asn Cys Arg Leu
900 905 910
Val Pro Asn Pro Asp Gln Lys Asp Ser Asp Gly Asp Gly Arg Gly Asp
915 920 925
Ala Cys Lys Asp Asp Phe Asp His Asp Ser Val Pro Asp Ile Asp Asp
930 935 940
Ile Cys Pro Glu Asn Val Asp Ile Ser Glu Thr Asp Phe Arg Arg Phe

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Gln Met Ile Pro Leu Asp Pro Lys Gly Thr Ser Gln Asn Asp Pro Asn			
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Trp Val Val Arg His Gln Gly Lys Glu Leu Val Gln Thr Val Asn Cys			
	980	985	990
Asp Pro Gly Leu Ala Val Gly Tyr Asp Glu Phe Asn Ala Val Asp Phe			
	995	1000	1005
Ser Gly Thr Phe Phe Ile Asn Thr Glu Arg Asp Asp Asp Tyr Ala Gly			
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Phe Val Phe Gly Tyr Gln Ser Ser Ser Arg Phe Tyr Val Val Met Trp			
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			1040
Lys Gln Val Thr Gln Ser Tyr Trp Asp Thr Asn Pro Thr Arg Ala Gln			
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Gly Tyr Ser Gly Leu Ser Val Lys Val Val Asn Ser Thr Thr Gly Pro			
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Gly Glu His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr Pro Gly			
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Gln Val Arg Thr Leu Trp His Asp Pro Arg His Ile Gly Trp Lys Asp			
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Phe Thr Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe			
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			1120
Ile Arg Val Val Met Tyr Glu Gly Lys Lys Ile Met Ala Asp Ser Gly			
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Pro Ile Tyr Asp Lys Thr Tyr Ala Gly Gly Arg Leu Gly Leu Phe Val			
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gac tcg gag gga cat ctc tac acc gtt ccc atc cgg gaa cag ggc aac 103

Asp Ser Glu Gly His Leu Tyr Thr Val Pro Ile Arg Glu Gln Gly Asn

10

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atc tac aag ccc aac aac aag gcc atg gca gac gag ctg agc gag aag 151

Ile Tyr Lys Pro Asn Asn Lys Ala Met Ala Asp Glu Leu Ser Glu Lys

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caa gtg tac gac gcg cac acc aag gag atc gac ctg gtc aac cgc gac 199

Gln Val Tyr Asp Ala His Thr Lys Glu Ile Asp Leu Val Asn Arg Asp

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cct aaa cac ctc aac gat gac gtg gtc aag att gac ttt gaa gat gtg 247

Pro Lys His Leu Asn Asp Asp Val Val Lys Ile Asp Phe Glu Asp Val

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75

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Ser Phe Thr Thr Phe Thr Val Thr Lys Tyr Trp Phe Tyr Arg Leu Leu

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tct gcc ctc ttt ggc atc ccg atg gca ctc atc tgg ggc att tac ttc 391

Ser Ala Leu Phe Gly Ile Pro Met Ala Leu Ile Trp Gly Ile Tyr Phe

105

110

115

gcc att ctc tct ttc ctg cac atc tgg gca gtt gta cca tgc att aag 439

Ala Ile Leu Ser Phe Leu His Ile Trp Ala Val Val Pro Cys Ile Lys

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Val His Thr Val Cys Asp Pro Leu Phe Glu Ala Val Gly Lys Ile Phe
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Lys Ile Asp Phe Glu Asp Val Ile Ala Glu Pro Glu Gly Thr His Ser
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Phe His Gly Ile Trp Lys Ala Ser Phe Thr Thr Phe Thr Val Thr Lys
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Tyr Trp Phe Tyr Arg Leu Leu Ser Ala Leu Phe Gly Ile Pro Met Ala

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Leu Ile Trp Gly Ile Tyr Phe Ala Ile Leu Ser Phe Leu His Ile Trp

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Ala Val Val Pro Cys Ile Lys Ser Phe Leu Ile Glu Ile Gln Cys Thr

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Ser Arg Val Tyr Ser Ile Tyr Val His Thr Val Cys Asp Pro Leu Phe

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Lys	Trp	Glu	Leu	Tyr	Ile	Pro	Pro	Lys	Gln	Asn	Lys	Ser	Val	Leu	Val	
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Thr	Ile	Ala	Glu	Asp	Val	Ser	Gly	Met	Pro	Ala	Leu	Cys	Ser	Pro	Ile		
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<213> Homo sapiens

<400> 106

Met Ala Ala Pro Met Thr Pro Ala Ala Arg Pro Glu Asp Tyr Glu Ala
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Ala Leu Asn Ala Ala Leu Ala Asp Val Pro Glu Leu Ala Arg Leu Leu
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Glu Ile Asp Pro Tyr Leu Lys Pro Tyr Ala Val Asp Phe Gln Arg Arg
35 40 45
Tyr Lys Gln Phe Ser Gln Ile Leu Lys Asn Ile Gly Glu Asn Glu Gly
50 55 60
Gly Ile Asp Lys Phe Ser Arg Gly Tyr Glu Ser Phe Gly Val His Arg
65 70 75 80
Cys Ala Asp Gly Gly Leu Tyr Ser Lys Glu Trp Ala Pro Gly Ala Glu
85 90 95
Gly Val Phe Leu Thr Gly Asp Phe Asn Gly Trp Asn Pro Phe Ser Tyr
100 105 110
Pro Tyr Lys Lys Leu Asp Tyr Gly Lys Trp Glu Leu Tyr Ile Pro Pro

115 120 1241.22 125
 Lys Gln Asn Lys Ser Val Leu Val Pro His Gly Ser Lys Leu Lys Val
 130 135 140
 Val Ile Thr Ser Lys Ser Gly Glu Ile Leu Tyr Arg Ile Ser Pro Trp
 145 150 155 160
 Ala Lys Tyr Val Val Arg Glu Gly Asp Asn Val Asn Tyr Asp Trp Ile
 165 170 175
 His Trp Asp Pro Glu His Ser Tyr Glu Phe Lys His Ser Arg Pro Lys
 180 185 190
 Lys Pro Arg Ser Leu Arg Ile Tyr Glu Ser His Val Gly Ile Ser Ser
 195 200 205
 His Glu Gly Lys Val Ala Ser Tyr Lys His Phe Thr Cys Asn Val Leu
 210 215 220
 Pro Arg Ile Lys Gly Leu Gly Tyr Asn Cys Ile Gln Leu Met Ala Ile
 225 230 235 240
 Met Glu His Ala Tyr Tyr Ala Ser Phe Gly Tyr Gln Ile Thr Ser Phe
 245 250 255
 Phe Ala Ala Ser Ser Arg Tyr Gly Thr Pro Glu Glu Leu Gln Glu Leu
 260 265 270
 Val Asp Thr Ala His Ser Met Gly Ile Ile Val Leu Leu Asp Val Val
 275 280 285
 His Ser His Ala Ser Lys Asn Ser Ala Asp Gly Leu Asn Met Phe Asp
 290 295 300
 Gly Thr Asp Ser Cys Tyr Phe His Ser Gly Pro Arg Gly Thr His Asp
 305 310 315 320
 Leu Trp Asp Ser Arg Leu Phe Ala Tyr Ser Ser Trp Glu Val Leu Arg
 325 330 335
 Phe Leu Leu Ser Asn Ile Arg Trp Trp Leu Glu Glu Tyr Arg Phe Asp
 340 345 350
 Gly Phe Arg Phe Asp Gly Val Thr Ser Met Leu Tyr His His His Gly
 355 360 365
 Val Gly Gln Gly Phe Ser Gly Asp Tyr Ser Glu Tyr Phe Gly Leu Gln

1241.22

370 375 380
Val Asp Glu Asp Ala Leu Thr Tyr Leu Met Leu Ala Asn His Leu Val
385 390 395 400
His Thr Leu Cys Pro Asp Ser Ile Thr Ile Ala Glu Asp Val Ser Gly
405 410 415
Met Pro Ala Leu Cys Ser Pro Ile Ser Gln Gly Gly Gly Gly Phe Asp
420 425 430
Tyr Arg Leu Ala Met Ala Ile Pro Asp Lys Trp Ile Gln Leu Leu Lys
435 440 445
Glu Phe Lys Asp Glu Asp Trp Asn Met Gly Asp Ile Val Tyr Thr Leu
450 455 460
Thr Asn Arg Arg Tyr Leu Glu Lys Cys Ile Ala Tyr Ala Glu Ser His
465 470 475 480
Asp Gln Ala Leu Val Gly Asp Lys Ser Leu Ala Phe Trp Leu Met Asp
485 490 495
Ala Glu Met Tyr Thr Asn Met Ser Val Leu Thr Pro Phe Thr Pro Val
500 505 510
Ile Asp Arg Gly Ile Gln Leu His Lys Met Ile Arg Leu Ile Thr His
515 520 525
Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly
530 535 540
His Pro Glu Trp Leu Asp Phe Pro Arg Lys Gly Asn Asn Glu Ser Tyr
545 550 555 560
His Tyr Ala Arg Arg Gln Phe His Leu Thr Asp Asp Asp Leu Leu Arg
565 570 575
Tyr Lys Phe Leu Asn Asn Phe Asp Arg Asp Met Asn Arg Leu Glu Glu
580 585 590
Arg Tyr Gly Trp Leu Ala Ala Pro Gln Ala Tyr Val Ser Glu Lys His
595 600 605
Glu Gly Asn Lys Ile Ile Ala Phe Glu Arg Ala Gly Leu Leu Phe Ile
610 615 620

1241.22

tct cat gag gag agg gaa cat gct gag aaa ctg atg aag ctg cag aac	302
Ser His Glu Glu Arg Glu His Ala Glu Lys Leu Met Lys Leu Gln Asn	
60 65 70 75	
caa cga ggt ggc cga atc ttc ctt cag gat atc aag aaa cca gac tgt	350
Gln Arg Gly Gly Arg Ile Phe Leu Gln Asp Ile Lys Lys Pro Asp Cys	
80 85 90	
gat gac tgg gag agc ggg ctg aat gca atg gag tgt gca tta cat ttg	398
Asp Asp Trp Glu Ser Gly Leu Asn Ala Met Glu Cys Ala Leu His Leu	
95 100 105	
gaa aaa aat gtg aat cag tca cta ctg gaa ctg cac aaa ctg gcc act	446
Glu Lys Asn Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr	
110 115 120	
gac aaa aat gac ccc cat ttg tgt gac ttc att gag aca cat tac ctg	494
Asp Lys Asn Asp Pro His Leu Cys Asp Phe Ile Glu Thr His Tyr Leu	
125 130 135	
aat gag cag gtg aaa gcc atc aaa gaa ttg ggt gac cac gtg acc aac	542
Asn Glu Gln Val Lys Ala Ile Lys Glu Leu Gly Asp His Val Thr Asn	
140 145 150 155	
ttg cgc aag atg gga gcg ccc gaa tct ggc ttg gcg gaa tat ctc ttt	590
Leu Arg Lys Met Gly Ala Pro Glu Ser Gly Leu Ala Glu Tyr Leu Phe	
160 165 170	
gac aag cac acc ctg gga gac agt gat aat gaa agc taagcctcgg	636
Asp Lys His Thr Leu Gly Asp Ser Asp Asn Glu Ser	
175 180	
gctaattttcc ccatagccgt ggggtgactt ccctgggtcac caaggcagtg catgcatgtt	696
gggggtttcct ttaccttttc tataagttgt accaaaacat ccacttaagt tctttgattt	756
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<210> 108

<211> 183

<212> PRT

<213> Homo sapiens

1241.22

<400> 108

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20 25 30
Tyr Val Tyr Leu Ser Met Ser Tyr Tyr Phe Asp Arg Asp Asp Val Ala
35 40 45
Leu Lys Asn Phe Ala Lys Tyr Phe Leu His Gln Ser His Glu Glu Arg
50 55 60
Glu His Ala Glu Lys Leu Met Lys Leu Gln Asn Gln Arg Gly Gly Arg
65 70 75 80
Ile Phe Leu Gln Asp Ile Lys Lys Pro Asp Cys Asp Asp Trp Glu Ser
85 90 95
Gly Leu Asn Ala Met Glu Cys Ala Leu His Leu Glu Lys Asn Val Asn
100 105 110
Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn Asp Pro
115 120 125
His Leu Cys Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys
130 135 140
Ala Ile Lys Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly
145 150 155 160
Ala Pro Glu Ser Gly Leu Ala Glu Tyr Leu Phe Asp Lys His Thr Leu
165 170 175
Gly Asp Ser Asp Asn Glu Ser
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<210> 109

<211> 3460

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

1241.22

<222> (256)..(1857)

<220>

<221>

<222> 448,

<223> unknown

<400> 109

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gggctgggct gtgcgcctgc gcagtgtggg tcgctcccga ttccctgccc cggccggccc 180
cgcctcggct ccgcaccctc gccccgctct cagccgccgc tctgccccgc agcagccagc 240
cccgtgtccg gcagt atg ttc agc tgg gtc agc aag gat gcc cgc cgc aag 291
      Met Phe Ser Trp Val Ser Lys Asp Ala Arg Arg Lys
              1              5              10
aag gag ccg gag ctc ttc cag acg gtg gcc gag ggg ctg cgg cag ctg 339
Lys Glu Pro Glu Leu Phe Gln Thr Val Ala Glu Gly Leu Arg Gln Leu
              15              20              25
tac gcg cag aag ctg cta ccc ctg gag gag cac tac cgc ttc cac gag 387
Tyr Ala Gln Lys Leu Leu Pro Leu Glu Glu His Tyr Arg Phe His Glu
              30              35              40
ttc cac tcg ccc gcr ctg gag gac gct gac ttc gac aac aag cct atg 435
Phe His Ser Pro Xaa Leu Glu Asp Ala Asp Phe Asp Asn Lys Pro Met
              45              50              55              60
gtg ctc ctc gtg rgg cag tac agc acg ggc aag acc acc ttc atc cga 483
Val Leu Leu Val Xaa Gln Tyr Ser Thr Gly Lys Thr Thr Phe Ile Arg
              65              70              75
cac ctg atc gag cag gac ttc ccg ggg atg cgc atc ggg ccc gag ccc 531
His Leu Ile Glu Gln Asp Phe Pro Gly Met Arg Ile Gly Pro Glu Pro
              80              85              90
acc acc gac tcc ttc atc gcc gtc atg cac ggc ccc act gag ggc gtg 579
Thr Thr Asp Ser Phe Ile Ala Val Met His Gly Pro Thr Glu Gly Val
              95              100              105
gtg ccg ggc aac gcg ctc gtg gtg gac ccg cgg cgc ccc ttc cgc aag 627
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1241.22

Val	Pro	Gly	Asn	Ala	Leu	Val	Val	Asp	Pro	Arg	Arg	Pro	Phe	Arg	Lys	
110						115						120				
ctc	aac	gcg	ttt	ggc	aac	gct	ttc	ctc	aac	agg	ttc	atg	tgt	gcc	cag	675
Leu	Asn	Ala	Phe	Gly	Asn	Ala	Phe	Leu	Asn	Arg	Phe	Met	Cys	Ala	Gln	
125					130					135					140	
ctg	ccc	aac	ccc	gtc	ctg	gac	agc	atc	agc	atc	atc	gac	acc	ccc	ggg	723
Leu	Pro	Asn	Pro	Val	Leu	Asp	Ser	Ile	Ser	Ile	Ile	Asp	Thr	Pro	Gly	
					145					150					155	
atc	ctg	tct	gga	gag	aag	cag	cgg	atc	agc	aga	ggc	tat	gac	ttt	gca	771
Ile	Leu	Ser	Gly	Glu	Lys	Gln	Arg	Ile	Ser	Arg	Gly	Tyr	Asp	Phe	Ala	
					160					165					170	
gcc	gtc	ctg	gag	tgg	ttc	gcg	gag	cgt	gtg	gac	cgc	atc	atc	ctg	ctc	819
Ala	Val	Leu	Glu	Trp	Phe	Ala	Glu	Arg	Val	Asp	Arg	Ile	Ile	Leu	Leu	
					175					180					185	
ttc	gac	gcc	cac	aag	ctg	gac	atc	tcc	gat	gag	ttc	tcg	gaa	gtg	atc	867
Phe	Asp	Ala	His	Lys	Leu	Asp	Ile	Ser	Asp	Glu	Phe	Ser	Glu	Val	Ile	
					190					195					200	
aag	gct	ctg	aag	aac	cat	gag	gac	aag	atc	cgc	gtg	gtg	ctg	aac	aag	915
Lys	Ala	Leu	Lys	Asn	His	Glu	Asp	Lys	Ile	Arg	Val	Val	Leu	Asn	Lys	
205					210					215					220	
gca	gac	cag	atc	gag	acg	cag	cag	ctg	atg	cgg	gtg	tac	ggg	gcc	ctc	963
Ala	Asp	Gln	Ile	Glu	Thr	Gln	Gln	Leu	Met	Arg	Val	Tyr	Gly	Ala	Leu	
					225					230					235	
atg	tgg	tcc	ctg	ggc	aag	atc	atc	aac	acc	ccc	gag	gtg	gtc	agg	gtc	1011
Met	Trp	Ser	Leu	Gly	Lys	Ile	Ile	Asn	Thr	Pro	Glu	Val	Val	Arg	Val	
					240					245					250	
tac	atc	ggc	tcc	ttc	tgg	tcc	cac	ccg	ctc	ctc	atc	ccc	gac	aac	cgc	1059
Tyr	Ile	Gly	Ser	Phe	Trp	Ser	His	Pro	Leu	Leu	Ile	Pro	Asp	Asn	Arg	
					255					260					265	
aag	ctc	ttt	gag	gcc	gag	gag	cag	gac	ctc	ttc	aag	gac	atc	cag	tca	1107
Lys	Leu	Phe	Glu	Ala	Glu	Glu	Gln	Asp	Leu	Phe	Lys	Asp	Ile	Gln	Ser	

			1241.22	
270	275		280	
ctg ccc cga aac gcc gcc ctc agg aag ctc aat gac ctg atc aag cgg				1155
Leu Pro Arg Asn Ala Ala Leu Arg Lys Leu Asn Asp Leu Ile Lys Arg				
285	290	295	300	
gca cgg ctg gcc aag gtt cac gcc tac atc atc agc tcc ctc aag aaa				1203
Ala Arg Leu Ala Lys Val His Ala Tyr Ile Ile Ser Ser Leu Lys Lys				
	305	310	315	
gag atg ccc aat gtc ttt ggt aaa gag agc aaa aag aaa gag ctg gtg				1251
Glu Met Pro Asn Val Phe Gly Lys Glu Ser Lys Lys Lys Glu Leu Val				
	320	325	330	
aac aac ctg gga gag atc tac cag aag att gag cgc gag cac cag atc				1299
Asn Asn Leu Gly Glu Ile Tyr Gln Lys Ile Glu Arg Glu His Gln Ile				
	335	340	345	
tcc cct ggg gac ttc ccg agc ctc cgc aag atg cag gaa ctc ctg cag				1347
Ser Pro Gly Asp Phe Pro Ser Leu Arg Lys Met Gln Glu Leu Leu Gln				
	350	355	360	
acc cag gac ttc agc aag ttc cag gcg ctg aag ccc aag ctg ctg gac				1395
Thr Gln Asp Phe Ser Lys Phe Gln Ala Leu Lys Pro Lys Leu Leu Asp				
365	370	375	380	
acg gtg gat gac atg ctg gcc aac gac atc gcg cgg ctg atg gtg atg				1443
Thr Val Asp Asp Met Leu Ala Asn Asp Ile Ala Arg Leu Met Val Met				
	385	390	395	
gtg cgg cag gag gag tcc ctg atg cct tcc cag gtg gtc aag ggc ggc				1491
Val Arg Gln Glu Glu Ser Leu Met Pro Ser Gln Val Val Lys Gly Gly				
	400	405	410	
gcc ttt gac ggc acc atg aac ggg ccg ttc ggg cac ggc tac ggc gag				1539
Ala Phe Asp Gly Thr Met Asn Gly Pro Phe Gly His Gly Tyr Gly Glu				
	415	420	425	
ggg gcc ggc gag ggc atc cac gac gtg gag tgg gtg gtg ggc aag gac				1587
Gly Ala Gly Glu Gly Ile His Asp Val Glu Trp Val Val Gly Lys Asp				
	430	435	440	
aag ccc acc tac gac gag atc ttc tac acg ctg tcc cct gtc aac ggc				1635

1241.22

Lys Pro Thr Tyr Asp Glu Ile Phe Tyr Thr Leu Ser Pro Val Asn Gly
445 450 455 460
aag atc acg ggc gcc aac gcc aag aag gag atg gtg aag tcc aag ctc 1683
Lys Ile Thr Gly Ala Asn Ala Lys Lys Glu Met Val Lys Ser Lys Leu
465 470 475
ccc aac acc gtg cta ggg aag atc tgg aag ctg gcc gac gtg gac aag 1731
Pro Asn Thr Val Leu Gly Lys Ile Trp Lys Leu Ala Asp Val Asp Lys
480 485 490
gac ggg ctg ctg gac gac gag gag ttc gcg ctg gcc aac cac ctc atc 1779
Asp Gly Leu Leu Asp Asp Glu Glu Phe Ala Leu Ala Asn His Leu Ile
495 500 505
aag gtc aag ctg gag ggc cac gag ctg ccc gcc gac ctg ccc ccg cac 1827
Lys Val Lys Leu Glu Gly His Glu Leu Pro Ala Asp Leu Pro Pro His
510 515 520
ctg gtg ccg ccc tcc aag cgc aga cat gag tgatggcgcc cggccccgca 1877
Leu Val Pro Pro Ser Lys Arg Arg His Glu
525 530
cctgccattt gcacgcccgg ccgggaggca gagacggggg gaggggaagc ctcaccattt 1937
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cctggacccc agtgttgcac ttcttggtg aggaagggtg gtcatcccag ctctgcccct 2777
accctctcac ttaactggag ctttgggacg caccctccac agtgggaggt ggtggtgggg 2837
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taggctctca tgtccagaca gcggggacca ggggaaaacc cagccccttc tgtaatcccc 2957
cttcatttcc taccttcctt cctcctctgt ttagcaaagg agggcagctc acttggaatgt 3017
ccttacaacg cccctggccc caggttgagc aataagaaac cagaaccttg cggcccagtg 3077
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caggggcccg ggtgcgtttg caagccagtg gccactgtcc gggctgtgat ggcaccaagg 3197
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ccgtcactcc atacagtatt aggtgaggat ggatgcgggc gctgtccttg ccgggaagtc 3377
actgttgaag ttgcagtggc ttgttcacac ctgtgggaag agaagtgaag actttctcct 3437
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<210> 110

<211> 534

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (49)

<223>

<220>

<221> unsure

<222> (65)

<223>

<400> 110

Met Phe Ser Trp Val Ser Lys Asp Ala Arg Arg Lys Lys Glu Pro Glu

1

5

10

15

Leu Phe Gln Thr Val Ala Glu Gly Leu Arg Gln Leu Tyr Ala Gln Lys

20

25

30

Leu Leu Pro Leu Glu Glu His Tyr Arg Phe His Glu Phe His Ser Pro

1241.22

35	40	45
Xaa Leu Glu Asp Ala Asp Phe Asp Asn Lys Pro Met Val Leu Leu Val		
50	55	60
Xaa Gln Tyr Ser Thr Gly Lys Thr Thr Phe Ile Arg His Leu Ile Glu		
65	70	75
Gln Asp Phe Pro Gly Met Arg Ile Gly Pro Glu Pro Thr Thr Asp Ser		
85	90	95
Phe Ile Ala Val Met His Gly Pro Thr Glu Gly Val Val Pro Gly Asn		
100	105	110
Ala Leu Val Val Asp Pro Arg Arg Pro Phe Arg Lys Leu Asn Ala Phe		
115	120	125
Gly Asn Ala Phe Leu Asn Arg Phe Met Cys Ala Gln Leu Pro Asn Pro		
130	135	140
Val Leu Asp Ser Ile Ser Ile Ile Asp Thr Pro Gly Ile Leu Ser Gly		
145	150	155
Glu Lys Gln Arg Ile Ser Arg Gly Tyr Asp Phe Ala Ala Val Leu Glu		
165	170	175
Trp Phe Ala Glu Arg Val Asp Arg Ile Ile Leu Leu Phe Asp Ala His		
180	185	190
Lys Leu Asp Ile Ser Asp Glu Phe Ser Glu Val Ile Lys Ala Leu Lys		
195	200	205
Asn His Glu Asp Lys Ile Arg Val Val Leu Asn Lys Ala Asp Gln Ile		
210	215	220
Glu Thr Gln Gln Leu Met Arg Val Tyr Gly Ala Leu Met Trp Ser Leu		
225	230	235
Gly Lys Ile Ile Asn Thr Pro Glu Val Val Arg Val Tyr Ile Gly Ser		
245	250	255
Phe Trp Ser His Pro Leu Leu Ile Pro Asp Asn Arg Lys Leu Phe Glu		
260	265	270
Ala Glu Glu Gln Asp Leu Phe Lys Asp Ile Gln Ser Leu Pro Arg Asn		
275	280	285
Ala Ala Leu Arg Lys Leu Asn Asp Leu Ile Lys Arg Ala Arg Leu Ala		

1241.22

290	295	300	
Lys Val His Ala Tyr Ile Ile Ser Ser Leu Lys Lys Glu Met Pro Asn			
305	310	315	320
Val Phe Gly Lys Glu Ser Lys Lys Lys Glu Leu Val Asn Asn Leu Gly			
	325	330	335
Glu Ile Tyr Gln Lys Ile Glu Arg Glu His Gln Ile Ser Pro Gly Asp			
	340	345	350
Phe Pro Ser Leu Arg Lys Met Gln Glu Leu Leu Gln Thr Gln Asp Phe			
	355	360	365
Ser Lys Phe Gln Ala Leu Lys Pro Lys Leu Leu Asp Thr Val Asp Asp			
370	375	380	
Met Leu Ala Asn Asp Ile Ala Arg Leu Met Val Met Val Arg Gln Glu			
385	390	395	400
Glu Ser Leu Met Pro Ser Gln Val Val Lys Gly Gly Ala Phe Asp Gly			
	405	410	415
Thr Met Asn Gly Pro Phe Gly His Gly Tyr Gly Glu Gly Ala Gly Glu			
	420	425	430
Gly Ile His Asp Val Glu Trp Val Val Gly Lys Asp Lys Pro Thr Tyr			
	435	440	445
Asp Glu Ile Phe Tyr Thr Leu Ser Pro Val Asn Gly Lys Ile Thr Gly			
450	455	460	
Ala Asn Ala Lys Lys Glu Met Val Lys Ser Lys Leu Pro Asn Thr Val			
465	470	475	480
Leu Gly Lys Ile Trp Lys Leu Ala Asp Val Asp Lys Asp Gly Leu Leu			
	485	490	495
Asp Asp Glu Glu Phe Ala Leu Ala Asn His Leu Ile Lys Val Lys Leu			
	500	505	510
Glu Gly His Glu Leu Pro Ala Asp Leu Pro Pro His Leu Val Pro Pro			
	515	520	525
Ser Lys Arg Arg His Glu			
530			

1241.22

<210> 111

<211> 1622

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (89)..(724)

<400> 111

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gtgtgattaa cctccatttc agctaatac atg gga gag att aaa gtc tct cct    112
                               Met Gly Glu Ile Lys Val Ser Pro
                               1             5
gat tat aac tgg ttt aga ggt aca gtt ccc ctt aaa aag att att gtg    160
Asp Tyr Asn Trp Phe Arg Gly Thr Val Pro Leu Lys Lys Ile Ile Val
    10             15             20
gat gat gat gac agt aag ata tgg tcg ctc tat gac gcg ggc ccc cga    208
Asp Asp Asp Asp Ser Lys Ile Trp Ser Leu Tyr Asp Ala Gly Pro Arg
    25             30             35             40
agt atc agg tgt cct ctc ata ttc ctg ccc cct gtc agt gga act gca    256
Ser Ile Arg Cys Pro Leu Ile Phe Leu Pro Pro Val Ser Gly Thr Ala
           45             50             55
gat gtc ttt ttc cgg cag att ttg gct ctg act gga tgg ggt tac cgg    304
Asp Val Phe Phe Arg Gln Ile Leu Ala Leu Thr Gly Trp Gly Tyr Arg
           60             65             70
gtt atc gct ttg cag tat cca gtt tat tgg gac cat ctc gag ttc tgt    352
Val Ile Ala Leu Gln Tyr Pro Val Tyr Trp Asp His Leu Glu Phe Cys
           75             80             85
gat gga ttc aga aaa ctt tta gac cat tta caa ttg gat aaa gtt cat    400
Asp Gly Phe Arg Lys Leu Leu Asp His Leu Gln Leu Asp Lys Val His
           90             95            100
ctt ttt ggc gct tct ttg gga ggc ttt ttg gcc cag aaa ttt gct gaa    448
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[illegible]

1241.22

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tctcctgcaa atcaactgct ttttaatttac acttaaacia attgttttga gtgttagcta 1574
ctgcctttct agatattagt cttttggaat aaaaattcaa tttcactg 1622

<210> 112

<211> 212

<212> PRT

<213> Homo sapiens

<400> 112

Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn Trp Phe Arg Gly Thr
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20 25 30
Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe
35 40 45
Leu Pro Pro Val Ser Gly Thr Ala Asp Val Phe Phe Arg Gln Ile Leu
50 55 60
Ala Leu Thr Gly Trp Gly Tyr Arg Val Ile Ala Leu Gln Tyr Pro Val
65 70 75 80
Tyr Trp Asp His Leu Glu Phe Cys Asp Gly Phe Arg Lys Leu Leu Asp
85 90 95
His Leu Gln Leu Asp Lys Val His Leu Phe Gly Ala Ser Leu Gly Gly
100 105 110
Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His Lys Ser Pro Arg Val
115 120 125
His Ser Leu Ile Leu Cys Asn Ser Phe Ser Asp Thr Ser Ile Phe Asn
130 135 140
Gln Thr Trp Thr Ala Asn Ser Phe Trp Leu Met Pro Ala Phe Met Leu
145 150 155 160
Lys Lys Ile Val Leu Gly Asn Phe Ser Ser Gly Pro Val Asp Pro Met
165 170 175
Met Ala Asp Ala Ile Asp Phe Met Val Asp Arg Leu Glu Ser Leu Gly

1241.22

180

185

190

Gln Ser Glu Leu Ala Ser Arg Leu Thr Leu Lys Leu Ser Lys Phe Leu

195

200

205

Cys Gly Thr Ser

210

<210> 113

<211> 2391

<212> DNA

<213> Homo sapiens

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<222> (1)..(360)

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1241.22

<222> (1705)

<223> g or t

<400> 113

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kcw tty kkc tcc aaa acg tgg att gag gtc tca ggt tcc tct scc aaa 96
Xaa Xaa Xaa Ser Lys Thr Trp Ile Glu Val Ser Gly Ser Ser Xaa Lys
      20             25             30
gat gyt kca aag cag ctg aag gag cag cag atg gtg atg aga ggc cac 144
Asp Xaa Xaa Lys Gln Leu Lys Glu Gln Gln Met Val Met Arg Gly His
      35             40             45
cga gag acc tcc atg gtc cat gaa ctc aac cgg tac atc ccc aca gcc 192
Arg Glu Thr Ser Met Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala
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gcg gcc ttt ggt ggg ctg tgc atc ggg gcc ctc tcg gtc ctg gct gac 240
Ala Ala Phe Gly Gly Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp
      65             70             75             80
ttc cta ggc gcc att ggg tct gga acc ggg atc ctg ctc gca gtc aca 288
Phe Leu Gly Ala Ile Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr
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atc atc tac cag tac ttt gag atc ttc gtt aag gag yaa agc gag gtt 336
Ile Ile Tyr Gln Tyr Phe Glu Ile Phe Val Lys Glu Xaa Ser Glu Val
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Gly Ser Met Gly Ala Leu Leu Phe
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1241.22

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1241.22

<212> PRT

<213> Homo sapiens

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<223> unknown

<400> 114

Asp Pro Phe His Ala Val Val Tyr Ile Val Phe Met Leu Gly Ser Cys

1

5

10

15

Xaa Xaa Xaa Ser Lys Thr Trp Ile Glu Val Ser Gly Ser Ser Xaa Lys

20

25

30

Asp Xaa Xaa Lys Gln Leu Lys Glu Gln Gln Met Val Met Arg Gly His

35

40

45

Arg Glu Thr Ser Met Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala

50

55

60

1241.22

Ala	Ala	Phe	Gly	Gly	Leu	Cys	Ile	Gly	Ala	Leu	Ser	Val	Leu	Ala	Asp
65					70					75					80
Phe	Leu	Gly	Ala	Ile	Gly	Ser	Gly	Thr	Gly	Ile	Leu	Leu	Ala	Val	Thr
				85					90					95	
Ile	Ile	Tyr	Gln	Tyr	Phe	Glu	Ile	Phe	Val	Lys	Glu	Xaa	Ser	Glu	Val
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Gly	Ser	Met	Gly	Ala	Leu	Leu	Phe								
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<210> 115

<211> 599

<212> DNA

<213> Homo sapiens

<400> 115

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agtgaggctg gagggagtta aggtcagtat ggaagatagg gttgggacag ggtgctttgg 180
aatgaaagag tgacctaga gggctccttg ggcctcagga atgctcctgc tgctgtgaag 240
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gaggactagc aggaggcagc cttgagaaac cggcagttcc caaagccagc gcctggctgt 480
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1241.22

<220>

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<223> a, c, g or t

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<221> unsure

<222> (179)

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cacagttcca gganngggta ggtagcagtg tgtgtgttat gtgccactga ccctgaaara 180

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gtaatcccag caccttgga agctgaggtg ggaggattgc ttgaaaccag gagttcaaga 300

ccagcctgtg caacatagca aaaccccatc tctacaaaga ttaaaaataa aaaattagct 360

gggc 364

<210> 117

<211> 852

<212> DNA

<213> Homo sapiens

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1241.22

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<223> a, c, g or t

<400> 117

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                               1           5
agc tgg gct aac ctt tcc cga act tgt ttc ccg gag gca agg tgc tcg 100
Ser Trp Ala Asn Leu Ser Arg Thr Cys Phe Pro Glu Ala Arg Cys Ser
 10           15           20           25
gtg acc cag cgc atc tta acc ttg ggt ctc cta ggc tcg agg cta ggg 148
Val Thr Gln Arg Ile Leu Thr Leu Gly Leu Leu Gly Ser Arg Leu Gly
          30           35           40
cat tac gtt tcg tgg aac caa agc agc caa ttg cat agc aag tat ttt 196
His Tyr Val Ser Trp Asn Gln Ser Ser Gln Leu His Ser Lys Tyr Phe
          45           50           55
cct gca ttc caa tta aat gct taagaaaaag cagcatccta taaaattgtg 247
Pro Ala Phe Gln Leu Asn Ala
          60
atcataaaca tccatttccc tcagcttttg tgagtgcctt gacttacagc caacatcact 307
gtttaactca gtctgtttta aaacaaactt ttctggtggt tgataacaga gagttgctcc 367
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cagctgttgg ctgaccagaa taaactccct gctgagttca agctttgaat ggaatggatg 487
caaatgatgt tgtttccatt agagcagggtg ctacacagcat tctgattggc ctgagcagac 547
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tgaatacatc acattcctat gcaaatgttt ttaatctcca gtttaatgta gtttattttt 787
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1241.22

<211> 64

<212> PRT

<213> Homo sapiens

<220>

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<400> 118

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Thr Cys Phe Pro Glu Ala Arg Cys Ser Val Thr Gln Arg Ile Leu Thr

20 25 30

Leu Gly Leu Leu Gly Ser Arg Leu Gly His Tyr Val Ser Trp Asn Gln

35 40 45

Ser Ser Gln Leu His Ser Lys Tyr Phe Pro Ala Phe Gln Leu Asn Ala

50 55 60

<210> 119

<211> 1156

<212> DNA

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<220>

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<222> (10)

<223> a or t

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gctagagaca gggagagcag agtaaaaccc tcaggctgct gaaatttcta ggctgttagg 180

1241.22

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 aagcaatagc agcaggagtc cccagcagct ggagccgcaa gaatgaactg caaagagggg 480
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Met Leu Lys Cys

1

gtg gtg gtg ggg gac ggt gcc gtg ggg aaa acc tgc ctg ctg atg agc 583
 Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys Leu Leu Met Ser
 5 10 15 20

tac gcc aac gac gcc ttc cca gag gaa tac gtg ccc act gtg ttt gac 631
 Tyr Ala Asn Asp Ala Phe Pro Glu Glu Tyr Val Pro Thr Val Phe Asp
 25 30 35

cac tat gca gtt act gtg act gtg gga ggc aag caa cac ttg ctc gga 679
 His Tyr Ala Val Thr Val Thr Val Gly Gly Lys Gln His Leu Leu Gly
 40 45 50

ctg tat gac acc gcg gga cag gag gac tac aac cag ctg agg cca ctc 727
 Leu Tyr Asp Thr Ala Gly Gln Glu Asp Tyr Asn Gln Leu Arg Pro Leu
 55 60 65

tcc tac ccc aac acg gat gtg ttt ttg atc tgc ttc tct gtc gta aac 775
 Ser Tyr Pro Asn Thr Asp Val Phe Leu Ile Cys Phe Ser Val Val Asn
 70 75 80

cct gcc tct tac cac aat gtc cag gag gaa tgg gtc ccc gag ctc aag 823
 Pro Ala Ser Tyr His Asn Val Gln Glu Glu Trp Val Pro Glu Leu Lys
 85 90 95 100

gac tgc atg cct cac gtg cct tat gtc ctc ata ggg acc cag att gat 871
 Asp Cys Met Pro His Val Pro Tyr Val Leu Ile Gly Thr Gln Ile Asp
 105 110 115

ctc cgt gat gac cca aaa acc ttg gcc cgt ttg ctg tat atg aaa gag 919
 Leu Arg Asp Asp Pro Lys Thr Leu Ala Arg Leu Leu Tyr Met Lys Glu

1241.22

120	125	130	
aaa cct ctc act tac gag cat ggt gtg aag ctc gca aaa gcg atc gga			967
Lys Pro Leu Thr Tyr Glu His Gly Val Lys Leu Ala Lys Ala Ile Gly			
135	140	145	
gca cag tgc tac ttg gaa tgt tca gct ctg act cag aaa ggt ctc aaa			1015
Ala Gln Cys Tyr Leu Glu Cys Ser Ala Leu Thr Gln Lys Gly Leu Lys			
150	155	160	
gcg gtt ttt gat gaa gca atc ctc acc att ttc cac ccc aag aaa aag			1063
Ala Val Phe Asp Glu Ala Ile Leu Thr Ile Phe His Pro Lys Lys Lys			
165	170	175	180
aag aaa cgc tgt tct gag ggt cac agc tgc tgt tca att atc			1105
Lys Lys Arg Cys Ser Glu Gly His Ser Cys Cys Ser Ile Ile			
185	190		
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<210> 120

<211> 194

<212> PRT

<213> Homo sapiens

<400> 120

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Leu Leu Met Ser Tyr Ala Asn Asp Ala Phe Pro Glu Glu Tyr Val Pro	
20 25 30	
Thr Val Phe Asp His Tyr Ala Val Thr Val Thr Val Gly Gly Lys Gln	
35 40 45	
His Leu Leu Gly Leu Tyr Asp Thr Ala Gly Gln Glu Asp Tyr Asn Gln	
50 55 60	
Leu Arg Pro Leu Ser Tyr Pro Asn Thr Asp Val Phe Leu Ile Cys Phe	
65 70 75 80	
Ser Val Val Asn Pro Ala Ser Tyr His Asn Val Gln Glu Glu Trp Val	
85 90 95	

1241.22

Pro Glu Leu Lys Asp Cys Met Pro His Val Pro Tyr Val Leu Ile Gly
100 105 110

Thr Gln Ile Asp Leu Arg Asp Asp Pro Lys Thr Leu Ala Arg Leu Leu
115 120 125

Tyr Met Lys Glu Lys Pro Leu Thr Tyr Glu His Gly Val Lys Leu Ala
130 135 140

Lys Ala Ile Gly Ala Gln Cys Tyr Leu Glu Cys Ser Ala Leu Thr Gln
145 150 155 160

Lys Gly Leu Lys Ala Val Phe Asp Glu Ala Ile Leu Thr Ile Phe His
165 170 175

Pro Lys Lys Lys Lys Lys Arg Cys Ser Glu Gly His Ser Cys Cys Ser
180 185 190

Ile Ile

<210> 121

<211> 1732

<212> DNA

<213> Homo sapiens

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<222> (388)

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<222> (631)

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<222> (639)

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1

5

10

15

acc gtg tat gcc ctg gcg gtc atc tcg acg cca gac cag acc aaa gtc 97

Thr Val Tyr Ala Leu Ala Val Ile Ser Thr Pro Asp Gln Thr Lys Val

20

25

30

ttc agt gca tcc tac gac cgg tcc ctc agg gtc tgg agt atg gac aac 145

Phe Ser Ala Ser Tyr Asp Arg Ser Leu Arg Val Trp Ser Met Asp Asn

35

40

45

atg atc tgc acg cag acc ctg ctg cgt cac cag ggc agt gtc acc gcg 193

Met Ile Cys Thr Gln Thr Leu Leu Arg His Gln Gly Ser Val Thr Ala

50

55

60

ctg gct gtg tcc cgg ggc cga ctc ttc tca ggg gct gtg gat agc act 241

Leu Ala Val Ser Arg Gly Arg Leu Phe Ser Gly Ala Val Asp Ser Thr

65

70

75

80

gtg aag gtt tgg act tgc taacaggatc caggccaggc tgtggtttcc 289

Val Lys Val Trp Thr Cys

85

1241.22

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<210> 122

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

1241.22

<222> (9)

<223> unknown

<400> 122

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20 25 30
Phe Ser Ala Ser Tyr Asp Arg Ser Leu Arg Val Trp Ser Met Asp Asn
35 40 45
Met Ile Cys Thr Gln Thr Leu Leu Arg His Gln Gly Ser Val Thr Ala
50 55 60
Leu Ala Val Ser Arg Gly Arg Leu Phe Ser Gly Ala Val Asp Ser Thr
65 70 75 80
Val Lys Val Trp Thr Cys
85

<210> 123

<211> 603

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (168)..(350)

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<223> g or a

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<222> (422)

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1241.22

<221> unsure

<222> (457)

<223> g or c

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gccaaacttg gttgaagact aggtcttccc tggcaagttc cggaaga atg gac tta 176

Met Asp Leu

1

ctg act ttt atc aac tct tct cac tgc caa ggc caa cag cat ctg agg 224
Leu Thr Phe Ile Asn Ser Ser His Cys Gln Gly Gln Gln His Leu Arg

5

10

15

tat agc ttt ttg gga gta cct gct ttc ttg cct cct gga gga tat ttt 272
Tyr Ser Phe Leu Gly Val Pro Ala Phe Leu Pro Pro Gly Gly Tyr Phe

20

25

30

35

ctg tcc tgg ggc ttc atg gcc cct ctc ttc cct gtt aca cat tgc tgt 320
Leu Ser Trp Gly Phe Met Ala Pro Leu Phe Pro Val Thr His Cys Cys

40

45

50

gct tca gag cct ttg cag ctg cra cct agt tgaatccaca taggsttcct 370
Ala Ser Glu Pro Leu Gln Leu Xaa Pro Ser

55

60

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ggaggtgggt ttttgttccc ttcaggsctt tggcaacatc tagagacagt tttgattgcc 490
acgcctggag tgggatgtgt gtgctactgg catctagtgg ctgctaaaca tcctacactg 550
cataggatag tccccactac cccagccaa gaattatctg actccagggg tca 603

<210> 124

<211> 61

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

1241.22

<222> (59)

<223> unknown

<400> 124

Met Asp Leu Leu Thr Phe Ile Asn Ser Ser His Cys Gln Gly Gln Gln

1 5 10 15

His Leu Arg Tyr Ser Phe Leu Gly Val Pro Ala Phe Leu Pro Pro Gly

20 25 30

Gly Tyr Phe Leu Ser Trp Gly Phe Met Ala Pro Leu Phe Pro Val Thr

35 40 45

His Cys Cys Ala Ser Glu Pro Leu Gln Leu Xaa Pro Ser

50 55 60

<210> 125

<211> 1289

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (775)..(1017)

<220>

<221> unsure

<222> (200)

<223> g or a

<400> 125

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ctttatagga aactatTTTT taaaaaaagc catttccac ccaaggacac agtggatgtg 120
ttttccctga ctccagcagg gcaaggaatg taaccgagag gttgtgtggg ctgggctctg 180
gtgccctctt ccctggcccr gaacacctct cctcctgatt cccttggcac cttgtctttc 240
tgtctgttta cctgtctccc tgccctgcca tctgcattct ttgcagccca ctctgacttc 300
catctggggg ctgagaccac ccttgccctgc ccccttcttt ctgccttaag aatgtccttt 360
taggctgggc atggttgtca cgcctgtaac ccagcactt tgggaggcgg agacgggcag 420
ataacctgag gtcaggattt cgagaccaac ctgacctaca tggagaaact ccgcctctag 480

1241.22

taaaaataca aaattagccg ggcattggtgg tgcacgcctc taatcccagc tactcgggag 540
gctgaggcag gagaatcact tgaacccggg aagtggaggt tgcagtgagc caagagtaca 600
ccactgcact ccagcctggg caacagagcg agactccgtc ttaaaaaaaaa aaaaaaaaaag 660
aacgcccttt tactgtcctc atcatcccag tttgaggcag tgctggagtg gggaaggccg 720
tcttagacca tagaggttgg aagacgctga gagatcatcc agcccagccc cttg atg 777
Met
1
tta cag agc aga aga cag atg ccc aaa cag gag aag gca ctt gcc cac 825
Leu Gln Ser Arg Arg Gln Met Pro Lys Gln Glu Lys Ala Leu Ala His
5 10 15
ggc cat acg gca ggt tgc cac aaa acc aag atg gca gcc ctt cct cag 873
Gly His Thr Ala Gly Cys His Lys Thr Lys Met Ala Ala Leu Pro Gln
20 25 30
cgt gcc tca ctg cca ctc cca gag cca ggg agc ccc ata aaa ccc aca 921
Arg Ala Ser Leu Pro Leu Pro Glu Pro Gly Ser Pro Ile Lys Pro Thr
35 40 45
tca tgt ctt aag agt ata tct ggc tcc ttg acc agc aat cgg ccc tgg 969
Ser Cys Leu Lys Ser Ile Ser Gly Ser Leu Thr Ser Asn Arg Pro Trp
50 55 60 65
gag cca cca ggt ggg aaa agc gcc tct gcc aga gtc cag gcc ttg gga 1017
Glu Pro Pro Gly Gly Lys Ser Ala Ser Ala Arg Val Gln Ala Leu Gly
70 75 80
tgacagacag cttgcccgc cactcgggcc ccactcaagg atgtagggcc ttttctggcc 1077
cctgaccctt ccctgggcat tgggagcgtg gggacggggc tggccttggg aggagcggca 1137
ggggcatcac ctcttctgc tgcttctccc tgctcctacc ctcaagggcc tgggggctgc 1197
ccagctgcct ctatgccctt ctgggggtct cagcccactg ctgacacttc tgcaatccag 1257
agaaacacta aataaagcaa tacgtgtttg cc 1289

<210> 126

<211> 81

<212> PRT

<213> Homo sapiens

1241.22

<400> 126

Met Leu Gln Ser Arg Arg Gln Met Pro Lys Gln Glu Lys Ala Leu Ala
1 5 10 15
His Gly His Thr Ala Gly Cys His Lys Thr Lys Met Ala Ala Leu Pro
20 25 30
Gln Arg Ala Ser Leu Pro Leu Pro Glu Pro Gly Ser Pro Ile Lys Pro
35 40 45
Thr Ser Cys Leu Lys Ser Ile Ser Gly Ser Leu Thr Ser Asn Arg Pro
50 55 60
Trp Glu Pro Pro Gly Gly Lys Ser Ala Ser Ala Arg Val Gln Ala Leu
65 70 75 80
Gly

<210> 127

<211> 1085

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (734)..(886)

<220>

<221> unsure

<222> (276)

<223> g or t

<400> 127

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ggaattacag gcacgcacca ccatgcctga ctaattttgt attttttagta gacatgggggt 180
ttctccatgt tggctcaggct ggtctcaaac tcccaccttc aggtgatccg cccacctcgg 240
cctcctgagg tggctgagat tacaggcgtg caactkgtgc cagcttgcta attttcacag 300
aagttgatgg caattcttca catgtaaaca gtgccagtgc acagaacctt tatatatattt 360

1241.22

ttgaagccag tactgtgctc tgcatataac aaagctgctt caaggatgag acctttttct 420
aaaagcatgt aatgtgagaa gccggcctgc cttattttct tttttctttt ttaatgatta 480
aaaatagttt gtggcaaggc acggtggctc aggcctgtaa ttctagcact ttgggaggcc 540
gaggcaggag gattacttga gcctacaagt ttgatgggcc agcatgcaca gcatagcaag 600
actgcatctc tacagagagt aaaaaaatt acccgagtgt ggtgatgtgc atctgtaatc 660
tcagctactt gggaggctga ggtgagagga tcacttgagc ttgggtgagg tgaggctgca 720
gtgagtcctg atc atg ctg ctg cac tca atc ttg gac aac aga gca aga 769

Met Leu Leu His Ser Ile Leu Asp Asn Arg Ala Arg

1 5 10

ccc tgt ctc aaa aaa aaa aat ata tat ata tat ata tat tat ttt 817
Pro Cys Leu Lys Lys Lys Lys Asn Ile Tyr Ile Tyr Ile Tyr Tyr Phe

15 20 25

tat gag gtg aag tgc atc aaa ctt ggg aaa gat ttg agg agg ctg gga 865
Tyr Glu Val Lys Cys Ile Lys Leu Gly Lys Asp Leu Arg Arg Leu Gly

30 35 40

acc tcc tgg aaa acc act cct tgaagaaaga tatgagagac atttagaagt 916
Thr Ser Trp Lys Thr Thr Pro

45 50

gattcctgct ttcagaagga ggtggattca aatacatcaa aagtccttc ctctgctaag 976
tgtttatagt tcaatgaata atttcaatat ttgtatgtgt tcttgtcatt ttattttttt 1036
ctgaaaaact tccaaaaatt tgaaaataaa attacagcct tttcttctt 1085

<210> 128

<211> 51

<212> PRT

<213> Homo sapiens

<400> 128

Met Leu Leu His Ser Ile Leu Asp Asn Arg Ala Arg Pro Cys Leu Lys

1 5 10 15

Lys Lys Lys Asn Ile Tyr Ile Tyr Ile Tyr Tyr Phe Tyr Glu Val Lys

20 25 30

Cys Ile Lys Leu Gly Lys Asp Leu Arg Arg Leu Gly Thr Ser Trp Lys

1241.22

35

40

45

Thr Thr Pro

50

<210> 129

<211> 1544

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (1076)

<223> g or a

<400> 129

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ttgttaggaa ggatctggaa taatcttgaa ggggaagtcag agttttctcc ctgcctatta 120

acaaaaaccc aattttgttc atattgaagc atgaaataaa tgagagcaag gtagggccaa 180

attaactctt gtggacagtc cctaaaagtc cagttctaca tttgtgaaaa ttgtggtgcc 240

atgaattaag atggatgact ggaaaaaggt gttggagaaa gagttaaaga tgaggaagag 300

atatttttag tatatgaagt tatccaggga cttgatattc ataattcagt gctgtggaaa 360

tgaaaaaat gattgaagag gtggaacgga aatgacctta gggggaaaaa aaaggaccaa 420

agaagtctga ttaaaagttg aaatcagtat ttctgaattc aaattgcttg aatttcctaa 480

atagtcagta aaggatctaa tagaaccaga attatttggg tgaattctgc aggttttatg 540

1241.22

ggcttgtcac aacgtgaagg gctggaatgt atattaccaa atgggaattt ccattgtagg	600
tttttgctag tcccaccccc attttagcct aatttggtt aaacgcagta tggggagaat	660
tgttcccat ccatgtgttc tgaattcagc tcatctcca gcatatagat atatcctcct	720
ttaactccga ccagaaccct tcttcctgtg gcactccca cccatagacc ttcagatcat	780
ctccacacc ctggatctca ctctcctctt agtaacagag acactcctga ggttggactt	840
ccttgctttt ctctacttcc aaatcacaat ttcttacaac caagctttgt gctcccagat	900
aagcagggat gtactagggg aatgtaaaac tgcaaaactta aaaacctgca tcttcttgaa	960
gcatcagttt tacttaccaa atggtttaga gtcataagat gacctatttt tatataaaag	1020
ttatattata gaataaaatg ttcatacgca tagactgtta agataaaaaa ataggraatc	1080
ttgcaaggta attcttattt gcaagtgggt tatgtgttca ctctcctcta cctttatgggt	1140
attttggtgt tcacttacga agcatacaac tagaaccata tccaagcaga ctctggggtg	1200
ctgttaacc agggcctaga cttctagtgc ctctgaggca gaaccaaagg agcctgcact	1260
gggggaaatc ctttttctg cctgcctgtc tgctgtgac ctgtgtacgt attacaggct	1320
ttaggaccag ctgattgtta tgcttgagg atggttttga aacagaaaca atacttgttt	1380
actgtaggaa tcctatttat attatttttc agtcctgtga atgctgtgaa aagatttatt	1440
cctttgaggc caggaagctc ccaggcatat atgcttctag gttaggattg tcctgactca	1500

1241.22

ctaaagatgc caggatattg gggctgaggg gagtttgagg tggt 1544

<210> 130

<211> 508

<212> DNA

<213> Homo sapiens

<400> 130

tgaaatcagg gctggagctt tacttaggat tcacatggcc tcctaggaac catgggacaa 60

atgggaaaca ggttatcggg ggattcatga agtcagtga agtaattgct tcttttttgc 120

gggtgaactg aatgtatttc ttcaccaa at cttgatgtta acaattaaaa agaagaaatg 180

acatgcaagt aggtcttagc agaaaaatgc aggctgggca tgagtcatgt tgttaccctc 240

ccacatgctc ctacaatcca cagagatgcc tgtctgcagg ttcttgaagt tattgttagt 300

atttggtatc tcaaattttt cgtcactggt cacatgccac tttctctgtg cacagtggta 360

tcctcatttg ctttttaacc tacactgagg agtctttgtc aggttgcaact gattttccaa 420

ttctgcagta atgagtaagc tcacggcatg gggaagaaga cagtcagtcc aatgaagttc 480

tctaaattat ttttaacattg cctttgaa 508

<210> 131

<211> 1204

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (50)
 <223> g or t
 <220>
 <221> unsure
 <222> (54)
 <223> g or c
 <220>
 <221> unsure
 <222> (300)
 <223> g or c
 <220>
 <221> unsure
 <222> (407)
 <223> g or a
 <220>
 <221> unsure
 <222> (415)
 <223> a,c,g or t
 <220>
 <221> unsure
 <222> (417)
 <223> g or c

 <220>
 <221> unsure
 <222> (419)
 <223> t or c
 <220>
 <221> unsure
 <222> (430)
 <223> a or t
 <220>

<221> unsure

<222> (448)

<223> t or c

<220>

<221> unsure

<222> (449)

<223> g or t

<220>

<221> unsure

<222> (472)

<223> a, c, g or t

<400> 131

ggccccctggc aatttgccctc aagatggggg ttgaaaata actttacctk actsaaggag 60

tgtctggagc acctcctagt ctaagtctgc aagctccagt tcttgccata aacctatgcca 120

gtggccaccc ttgggctcag acagctctgg gccttttgac cacaagccag cccctcgccc 180

tctctgtggc atagtcttct ctgccccagg actgcagggc ggcttcctcc aaggcttcca 240

aggctcaaaa gaaatttggc tccatccaag aaggctccag ctcccctact ggccccctggs 300

ttcaggccca caccctggg ccagggccag agagtgtgtc tcaggagaat tcaatgggct 360

ctagagagac acacagaaag ttggggcatt tgggaaattt tcaaggrtgt atgtntsgyt 420

cacgtatggw gcaggttgtc ctgggtccykg ggtgcaggga agtgggctgc anggaagtgg 480

attggagggg agcttgagga atataaggag cgggggtgga gactcaggct atggacaagg 540

acagcccca ggttgggaag acctggcctt agtcgtcctc agcctagggg cagggcagtg 600

1241.22

aagaaagctc tccccgctcc tgctgtaatg acccagagta gcctccccag gccggcatct	660
tatgtgtgtc ttccaccatc ctcatggtgg cacttttcta ggcctgtctc ccagcattgt	720
gcaaggctcg gaagagaacc agggaagtga aactgggtga aaacagaaag ctcaatggat	780
gggctagggtt ccccagatca ttagggcaga gtttgcacgt cctctggtca ctggaatcca	840
cccagcccac gaatcatctc cctcttgaag gattttattt ctactgggtt ttggaacaaa	900
ctcctgctga gacccacag ccagaaactg aaagcagcag ctccccaaag cctggaaaat	960
ccctaagaga aggcctgggg caggaagtgg agtgacaggg gacaggtaga gagaaggggg	1020
cccaatggcc agggagtga ggaggtggcg ttgctgagag cagtctgcac atgcttctgt	1080
ctgagtgcag gaaggtgttc cagggtcgaa attacacttc tcgtacctgg agacgtgtt	1140
tgtgggagca ctgggctcat gcctggcaca caataggtct gcaataaacc atgggttaa	1200
cctg	1204

<210> 132

<211> 508

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (223)

<223> a, c, g or t

<220>

1241.22

<221> unsure

<222> (237)

<223> a, c, g or t

<220>

<221> unsure

<222> (380)

<223> a, c, g or t

<220>

<221> unsure

<222> (468)

<223> a, c, g or t

<400> 132

cccgggagaa tcacttcagc ctgggagatc aaggctgcag tgagctctga acgcaccact 60

acactccagc ctgggtgaca gagtgagatc ctgtctcaaa aaaagagaaa gaaaaccttt 120

gagattcttc cattttttaga gctgagagag cacttgtgaa acacacacac atgcacaaac 180

atataaacat gcatacaggc atgcacatgc acacacaaat acncatacac acacacnagc 240

acacacacac caccaccacc atcatcagag gaacttacag aaaaggggac atttatagat 300

tcctaggaat atgccaaagc ttttcaaagc ctctatggac agctcattcc ttaacttttc 360

ctcttttaaaa tcttttttan cttcttattt gcccagcca ctatcactgc ctcaggcagc 420

tgcaacgtta aacaattgcc actgattact ttcaacaaat aacctcanag aaaaggctgt 480

gtgtattgaa tgggtatcaa gtcacgtc 508

<210> 133

<211> 484

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (313)

<223> a,c,g or t

<220>

<221> unsure

<222> (336)

<223> g or c

<220>

<221> unsure

<222> (401)

<223> g or c

<400> 133

gtcgactcga gcggccgcgg accgtttttt ttttttttct ctccctctgcc ccttctaata 60

tcttgagag ggatggagac tgaagagtga gtttggtcct ccacttgatc cagggttcta 120

tttttgtttt ctacttcaaa gcgagaactt ggtactgtga ctttgataag aattgacttc 180

aggcccagca agatccctca tgcctgtaat cccagcactt tggggggcca aggcaggagg 240

attgcgtgag cccaggagtt cgagaccac ctgggcaaca tagggacctt gtctctacaa 300

aaaataaaat tanctgggtt tgatggtgca catcastggt cctggctact cgggaggcca 360

agggtgggagg aatgcttgag gatcggaggt caaggctgca stgagccaat attgtgccac 420

tgcattccag cctgggcaac agagtgagac actgtcttaa aaaaaaaaaa aaaaaacggt 480

ccgc

484

<210> 134

<211> 605

<212> DNA

<213> Homo sapiens

<400> 134

gctgcatgtc taaaattaca tggagttagt gtctattctt tttccccctt tgcagcaact 60

tacacagcat ttttaacacc ttttttttct agtttttttg ttcggttttg ttttccatca 120

ggaatttgag ttctctctaa cccagcttac tgtgggacat aggaaaactc agtagaaata 180

cctttggtga tcttgttgag ttttaagtctg atcttgatct taaactcagt aagccactat 240

ctgcaatttt gtacattata tagtattttg aagatatgga accttatgaa aaaaaaatag 300

caaattagtt ctttttcccc cagaggggaa agttatgttc tgcaaatagt gtgtgtctta 360

ttttactggt gaacagcaat tgctatttat ttttttattg cctagaactt caacatgttg 420

tataggaatc ctgtagtgcc actagttaaa tgccgaattc tcatctggat gttaccatca 480

aacatcagta cacttgatcat ttcacatgtg tttaatgtga cagtttttca gtactgtatg 540

tgtaatttc tacttttttt aatattttaa attgctttta aataaacata ttctcagttg 600

atccc 605

<210> 135

<211> 1786

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2)..(151)

<220>

<221> unsure

<222> (689)

<223> g or a

<400> 135

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Ala Arg Gly Ser Ser Ala Trp Gly Gln Val Leu Leu Cys Leu Leu Ser

1

5

10

15

tac ctc tct cca cag cag ggc tct caa aac cat ttt gat ccc cca ttg 97

Tyr Leu Ser Pro Gln Gln Gly Ser Gln Asn His Phe Asp Pro Pro Leu

20

25

30

gca gag ggt tcc cct ctt tac aga gtt cag tca tta aaa gca tgg atc 145

Ala Glu Gly Ser Pro Leu Tyr Arg Val Gln Ser Leu Lys Ala Trp Ile

35

40

45

agc tgt taatctcatt ggaggaggga actgtttcct gcattcattc atctgggaac 201

Ser Cys

50

cttcttgagt agccactgtc tgccagccac tgctctagag atgggaaaac agcacggaac 261

aaaaccaagg tctttcttcc agcgaattta tctccttcag gaagctgggt cctgccacca 321

acttagcagg caacagttct cctcccctag tgggcacagg gtaccagttt tgtaggaaaa 381

gtggtccagc aaaggaagaa agcagaccaa cccagctgcc ttaccttatt ctggggccat 441

tccccagcg atgagagctg ctcttgtttc tactgccacc atctcttctg gctgcacttc 501

acctgctgct tgagcttctg accttccttc agttccacca aatgaggaca ggaaatagca 561

gtcaagaccc ctgggccctg ctgagcgtga aacaggaagg caatgggatg agttgctggg 621

acggaagaat gggcctgggg cagaacaaat agggagcatt tgaaagcttc tggctgataa 681

atctccargg tgcattcccg ttgccacgcc tgccccatt aacctgctcc tggtaaatac 741

1241.22

tgatccagca gctgctccag gagaggccgt cttttttttc ccagccacgc tgtgtctttg 801
catgagactc cttggggcct gggcacagag agaaaagaat tgagactcag gaggctcagt 861
gggtgagaaa atgcaaagtg gcttcacaga cacagggctg tgggagcaga tcgacgggga 921
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ttctaactag tgctagggaa agtcctgaga cacgatcaca gccactgctt ggcatacagg 1161
gcctccaccc aataagcaaa ctggagattc ctcagcctct cgtggacacc cacatctcat 1221
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aaccactcc tcttgacaca ctggaatctg tattatatat atttttaaga aaatacaatg 1581
atggttgtct ggttttgttg tttttacagg tgttgtggaa taaaaactgt aagaaaatta 1641
agtatttaaa atgttccaat aaagtggggg tttttgttat tctaatatat tattgtgtac 1701
ctattgtaaa tatgaaacac tcctattttg caagctgagg acacaatttg tactgttggt 1761
atatataaat aaagtttact gaatt 1786

<210> 136

<211> 50

<212> PRT

<213> Homo sapiens

<400> 136

Ala Arg Gly Ser Ser Ala Trp Gly Gln Val Leu Leu Cys Leu Leu Ser
1 5 10 15
Tyr Leu Ser Pro Gln Gln Gly Ser Gln Asn His Phe Asp Pro Pro Leu
20 25 30
Ala Glu Gly Ser Pro Leu Tyr Arg Val Gln Ser Leu Lys Ala Trp Ile
35 40 45
Ser Cys
50

<210> 137

<211> 835

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (535)..(729)

<400> 137

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agttactaaa atttacacat cttaaaagtg tgtaaagtct taaatttcag aattaccatc 120
agaacctcaa ttgacattcc tttgaatagg ctaataagtg acaaataaga ttaataagat 180
ttttcaaaat cgccaggact ggtgaatata aatgatgatt gaactggaat aatattgggg 240
accaaatacaa atgaatgatt aaattatgaa gtcatatcc ttttgaaggt agttgcaaag 300
agacatttca aaactgccct aggccattgc agcatcctta gatgggacgc ataatcatta 360
ccttaaagca tcaccactca ttttgaccat atagatttta ttatgttagt ttaaaaggtc 420
aatcagcctc atgactttat agttatgtct tgtattttaa aacatttttt atacatttgg 480
ttatgttgat aaaccaaaaa catttgatta ataaaatatc tatttgaata aatt atg 537

Met

1

agc tat cct ttc aaa cag cta ttg gca agt ttt aaa ccc aaa ata tat 585
Ser Tyr Pro Phe Lys Gln Leu Leu Ala Ser Phe Lys Pro Lys Ile Tyr

5

10

15

aca cat agt tct gta ata aaa ctg ttt gac ttc tca agt aac atg act 633
Thr His Ser Ser Val Ile Lys Leu Phe Asp Phe Ser Ser Asn Met Thr

20

25

30

tcc tta ttt ctg aac agt act ggt tac ttt caa aat gaa ttt tta ttg 681
Ser Leu Phe Leu Asn Ser Thr Gly Tyr Phe Gln Asn Glu Phe Leu Leu

35

40

45

aga ttt tcc att aac tat ttt ttt caa aga ctc aaa ttt tgt acc aag 729
Arg Phe Ser Ile Asn Tyr Phe Phe Gln Arg Leu Lys Phe Cys Thr Lys

50

55

60

65

1241.22

taaatccagg ctttatgtac aaacatggtg tttgttttat ttggggctgg gggaggtata 789
tgatgagcag acttctcgga attcataata aattttctaa aagcct 835

<210> 138

<211> 65

<212> PRT

<213> Homo sapiens

<400> 138

Met Ser Tyr Pro Phe Lys Gln Leu Leu Ala Ser Phe Lys Pro Lys Ile

1 5 10 15

Tyr Thr His Ser Ser Val Ile Lys Leu Phe Asp Phe Ser Ser Asn Met

20 25 30

Thr Ser Leu Phe Leu Asn Ser Thr Gly Tyr Phe Gln Asn Gln Phe Leu

35 40 45

Leu Arg Phe Ser Ile Asn Tyr Phe Phe Gln Arg Leu Lys Phe Cys Thr

50 55 60

Lys

65

<210> 139

<211> 626

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(201)

<220>

<221> unsure

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<220>

<221> unsure

1241.22

<222> (353)

<223> a or t

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<221> unsure

<222> (363)

<223> a or t

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<221> unsure

<222> (368)

<223> g or a

<400> 139

tgt ttc agt gtg act gtc ttg tta gag gtg aag ttt atc cag ggt aac 48

Cys Phe Ser Val Thr Val Leu Leu Glu Val Lys Phe Ile Gln Gly Asn

1

5

10

15

ttg ctc act aac tat tcc ttt tta tgg cct ggg gtt aaa ggg agc atg 96

Leu Leu Thr Asn Tyr Ser Phe Leu Trp Pro Gly Val Lys Gly Ser Met

20

25

30

gct cac act ggt gaa aat aag gaa ggc ctg gtc tta tct tgt att aat 144

Ala His Thr Gly Glu Asn Lys Glu Gly Leu Val Leu Ser Cys Ile Asn

35

40

45

aat act ggc tgc att cca cca gcc aga gat ttc tat ctg cga aga cct 192

Asn Thr Gly Cys Ile Pro Pro Ala Arg Asp Phe Tyr Leu Arg Arg Pro

50

55

60

atg aaa cac tgaagagaaa tgtaggcaga aggaaatggc cacatatcac 241

Met Lys His

65

aagttctatt atatattctt ttgtaaatac atattgtata ttacttggat gttttcttat 301

1241.22

atcatttact gtctttttga gttaatgtca gtttttactc tctcaaytta cwatgtwaca 361
twgtaartaa cataatgtcc tttattatatt atatttaagc atctaacata tagagttggt 421
ttcatataag ttttaagataa atgtcaaaaa tatatgttct tttgtttttc tttgctttaa 481
aattatgtat cttttccttt tctttttttt aagaataatt tattgttcag gagaaagaat 541
gtatatgtaa ctgaaactat ctgaagaatg cacattgaag gccgtgaggt actgataaac 601
taaagaattt attattcaaa atact 626

<210> 140

<211> 67

<212> PRT

<213> Homo sapiens

<400> 140

Cys Phe Ser Val Thr Val Leu Leu Glu Val Lys Phe Ile Gln Gly Asn

1 5 10 15

Leu Leu Thr Asn Tyr Ser Phe Leu Trp Pro Gly Val Lys Gly Ser Met

20 25 30

Ala His Thr Gly Glu Asn Lys Glu Gly Leu Val Leu Ser Cys Ile Asn

35 40 45

Asn Thr Gly Cys Ile Pro Pro Ala Arg Asp Phe Tyr Leu Arg Arg Pro

50 55 60

Met Lys His

65

<210> 141

<211> 525

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103)..(525)

<400> 141

aagaaatgga ggactcagaa ccaaggattt ccaagtgatt tcttccaaag cacaggaatc 60

1241.22

tcactctgtt aaagctgggc tgttctaact gagatgacag tc atg tcc ctt tcc	114
Met Ser Leu Ser	
1	
agg gac ctc aag gac gac ttt cac agt gac acg gta ctc tcc atc tta	162
Arg Asp Leu Lys Asp Asp Phe His Ser Asp Thr Val Leu Ser Ile Leu	
5 10 15 20	
aat gag cag cgc att cgg ggc att tta tgc gat gtc act atc att gtg	210
Asn Glu Gln Arg Ile Arg Gly Ile Leu Cys Asp Val Thr Ile Ile Val	
25 30 35	
gaa gat acc aaa ttt aaa gcc cat agc aat gtt ctg gca gct tca agc	258
Glu Asp Thr Lys Phe Lys Ala His Ser Asn Val Leu Ala Ala Ser Ser	
40 45 50	
ctg tat ttt aaa aat atc ttt tgg agc cat aca atc tgt att tcc agc	306
Leu Tyr Phe Lys Asn Ile Phe Trp Ser His Thr Ile Cys Ile Ser Ser	
55 60 65	
cac gtc ctg gag ctg gac gat ctc aaa gct gaa gtg ttt act gaa ata	354
His Val Leu Glu Leu Asp Asp Leu Lys Ala Glu Val Phe Thr Glu Ile	
70 75 80	
ctt aat tat atc tac agt tcc aca gtc gtt gtc aag aga cag gaa aca	402
Leu Asn Tyr Ile Tyr Ser Ser Thr Val Val Val Lys Arg Gln Glu Thr	
85 90 95 100	
gtc act gat ctc gca gct gca gga aaa aag ctg gga ata tcg ttc ttg	450
Val Thr Asp Leu Ala Ala Ala Gly Lys Lys Leu Gly Ile Ser Phe Leu	
105 110 115	
gaa gac ctt act gat cgc aac ttc tca aat tcc ccg ggt ccc tat gta	498
Glu Asp Leu Thr Asp Arg Asn Phe Ser Asn Ser Pro Gly Pro Tyr Val	
120 125 130	
ttc tgt att act gaa aag gga gtg gtt	525
Phe Cys Ile Thr Glu Lys Gly Val Val	
135 140	

<210> 142

1241.22

<211> 141

<212> PRT

<213> Homo sapiens

<400> 142

Met Ser Leu Ser Arg Asp Leu Lys Asp Asp Phe His Ser Asp Thr Val
1 5 10 15
Leu Ser Ile Leu Asn Glu Gln Arg Ile Arg Gly Ile Leu Cys Asp Val
20 25 30
Thr Ile Ile Val Glu Asp Thr Lys Phe Lys Ala His Ser Asn Val Leu
35 40 45
Ala Ala Ser Ser Leu Tyr Phe Lys Asn Ile Phe Trp Ser His Thr Ile
50 55 60
Cys Ile Ser Ser His Val Leu Glu Leu Asp Asp Leu Lys Ala Glu Val
65 70 75 80
Phe Thr Glu Ile Leu Asn Tyr Ile Tyr Ser Ser Thr Val Val Val Lys
85 90 95
Arg Gln Glu Thr Val Thr Asp Leu Ala Ala Ala Gly Lys Lys Leu Gly
100 105 110
Ile Ser Phe Leu Glu Asp Leu Thr Asp Arg Asn Phe Ser Asn Ser Pro
115 120 125
Gly Pro Tyr Val Phe Cys Ile Thr Glu Lys Gly Val Val
130 135 140

<210> 143

<211> 1827

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (138)..(1307)

<400> 143

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gtcgcgcagc ctcggcacct gcaggtccgt gcgtcccgcg gctggcgccc ctgactccgt 120
cccgccagg gagggcc atg att tcc ctc ccg ggg ccc ctg gtg acc aac 170
      Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn
            1             5             10
ttg ctg cgg ttt ttg ttc ctg ggg ctg agt gcc ctc gcg ccc ccc tcg 218
Leu Leu Arg Phe Leu Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser
            15             20             25
cgg gcc cag ctg caa ctg cac ttg ccc gcc aac cgg ttg cag gcg gtg 266
Arg Ala Gln Leu Gln Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val
            30             35             40
gag gga ggg gaa gtg gtg ctt cca gcg tgg tac acc ttg cac ggg gag 314
Glu Gly Gly Glu Val Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu
            45             50             55
gtg tct tca tcc cag cca tgg gag gtg ccc ttt gtg atg tgg ttc ttc 362
Val Ser Ser Ser Gln Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe
            60             65             70             75
aaa cag aaa gaa aag gag gat cag gtg ttg tcc tac atc aat ggg gtc 410
Lys Gln Lys Glu Lys Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val
            80             85             90
aca aca agc aaa cct gga gta tcc ttg gtc tac tcc atg ccc tcc cgg 458
Thr Thr Ser Lys Pro Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg
            95             100             105
aac ctg tcc ctg cgg ctg gag ggt ctc cag gag aaa gac tct ggc ccc 506
Asn Leu Ser Leu Arg Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro
            110             115             120
tac agc tgc tcc gtg aat gtg caa gac aaa caa ggc aaa tct agg ggc 554
Tyr Ser Cys Ser Val Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly
            125             130             135
cac agc atc aaa acc tta gaa ctc aat gta ctg gtt cct cca gct cct 602
His Ser Ile Lys Thr Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro
            140             145             150             155
cca tcc tgc cgt ctc cag ggt gtg ccc cat gtg ggg gca aac gtg acc 650

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1241.22

Pro Ser Cys Arg Leu Gln Gly Val	Pro His Val Gly Ala Asn Val Thr	
160	165	170
ctg agc tgc cag tct cca agg agt aag cct gct gtc caa tac cag tgg	698	
Leu Ser Cys Gln Ser Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp		
175	180	185
gat cgg cag ctt cca tcc ttc cag act ttc ttt gca cca gca tta gat	746	
Asp Arg Gln Leu Pro Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp		
190	195	200
gtc atc cgt ggg tct tta agc ctc acc aac ctt tcg tct tcc atg gct	794	
Val Ile Arg Gly Ser Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala		
205	210	215
gga gtc tat gtc tgc aag gcc cac aat gag gtg ggc act gcc caa tgt	842	
Gly Val Tyr Val Cys Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys		
220	225	230
aat gtg acg ctg gaa gtg agc aca ggg cct gga gct gca gtg gtt gct	890	
Asn Val Thr Leu Glu Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala		
240	245	250
gga gct gtt gtg ggt acc ctg gtt gga ctg ggg ttg ctg gct ggg ctg	938	
Gly Ala Val Val Gly Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu		
255	260	265
gtc ctc ttg tac cac cgc cgg ggc aag gcc ctg gag gag cca gcc aat	986	
Val Leu Leu Tyr His Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn		
270	275	280
gat atc aag gag gat gcc att gct ccc cgg acc ctg ccc tgg ccc aag	1034	
Asp Ile Lys Glu Asp Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys		
285	290	295
agc tca gac aca atc tcc aag aat ggg acc ctt tcc tct gtc acc tcc	1082	
Ser Ser Asp Thr Ile Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser		
300	305	310
gca cga gcc ctc tgg cca ccc cat ggc cct ccc agg cct ggt gca ttg	1130	
Ala Arg Ala Leu Trp Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu		

1241.22

320	325	330	
acc ccc acg ccc agt ctc tcc agc cag gcc ctg ccc tca cca aga ctg			1178
Thr Pro Thr Pro Ser Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu			
335	340	345	
ccc acg aca gat ggg gcc cac cct caa cca ata tcc ccc atc cct ggt			1226
Pro Thr Thr Asp Gly Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly			
350	355	360	
ggg gtt tct tcc tct ggc ttg agc cgc atg ggt gct gtg cct gtg atg			1274
Gly Val Ser Ser Ser Gly Leu Ser Arg Met Gly Ala Val Pro Val Met			
365	370	375	
gtg cct gcc cag agt caa gct ggc tct ctg gta tgatgacccc accactcatt			1327
Val Pro Ala Gln Ser Gln Ala Gly Ser Leu Val			
380	385	390	
ggctaaagga tttggggtct ctccttccta taagggtcac ctctagcaca gaggcctgag			1387
tcatgggaaa gagtcacact cctgaccctt agtactctgc cccacactct ctttactgtg			1447
ggaaaaccat ctgagtaaga cctaagtgtc caggagacag aaggagaaga ggaagtggat			1507
ctggaattgg gaggagcctc caccaccccc tgactcctcc ttatgaagcc agctgctgaa			1567
attagctact caccaagagt gaggggcaga gacttccagt cactgagtct cccaggcccc			1627
cttgatctgt accccacccc tatctaacac cacccttggc tcccactcca gctccctgta			1687
ttgatataac ctgtcaggct ggcttggtta ggttttactg gggcagagga tagggaatct			1747
cttattaaaa ctaacatgaa atatgtgttg ttttcatttg caaatttaaa taaagataca			1807
taatgtttgt atgagataag			1827

<210> 144

<211> 390

<212> PRT

<213> Homo sapiens

<400> 144

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1

5

10

15

Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln

20

25

30

1241.22

Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val
 35 40 45
 Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln
 50 55 60
 Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys
 65 70 75 80
 Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro
 85 90 95
 Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg
 100 105 110
 Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val
 115 120 125
 Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr
 130 135 140
 Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu
 145 150 155 160
 Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser
 165 170 175
 Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro
 180 185 190
 Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser
 195 200 205
 Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys
 210 215 220
 Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu
 225 230 235 240
 Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly
 245 250 255
 Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His
 260 265 270
 Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp
 275 280 285

1241.22

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile

290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Trp

305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser

325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly

340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser

355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser

370 375 380

Gln Ala Gly Ser Leu Val

385 390

<210> 145

<211> 3466

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (84)..(2726)

<400> 145

tgcggaagc gatgtagtag ctgccaggct gtcccccgcc ctgcccggcc cgagccccgc 60

gggccgccgc cgccaccgcc gcc atg aag aag cag ttc aac cgc atg aag cag 113

Met Lys Lys Gln Phe Asn Arg Met Lys Gln

1 5 10

ctg gct aac cag acc gtg ggc aga gct gag aaa aca gaa gtc ctt agt 161

Leu Ala Asn Gln Thr Val Gly Arg Ala Glu Lys Thr Glu Val Leu Ser

15 20 25

gaa gat cta tta cag att gag aga cgc ctg gac acg gtg cgg tca ata 209

Glu Asp Leu Leu Gln Ile Glu Arg Arg Leu Asp Thr Val Arg Ser Ile

1241.22

30	35	40	
tgc cac cat tcc cat aag cgc ttg gtg gca tgt ttc cag ggc cag cat	257		
Cys His His Ser His Lys Arg Leu Val Ala Cys Phe Gln Gly Gln His			
45	50	55	
ggc acc gat gcc gag agg aga cac aaa aaa ctg cct ctg aca gct ctt	305		
Gly Thr Asp Ala Glu Arg Arg His Lys Lys Leu Pro Leu Thr Ala Leu			
60	65	70	
gct caa aat atg caa gaa gca tcg act cag ctg gaa gac tct ctc ctg	353		
Ala Gln Asn Met Gln Glu Ala Ser Thr Gln Leu Glu Asp Ser Leu Leu			
75	80	85	90
ggg aag atg ctg gag acg tgt gga gat gct gag aat cag ctg gct ctc	401		
Gly Lys Met Leu Glu Thr Cys Gly Asp Ala Glu Asn Gln Leu Ala Leu			
95	100	105	
gag ctc tcc cag cac gaa gtc ttt gtt gag aag gag atc gtg gac cct	449		
Glu Leu Ser Gln His Glu Val Phe Val Glu Lys Glu Ile Val Asp Pro			
110	115	120	
ctg tac ggc ata gct gag gtg gag att ccc aac atc cag aag cag agg	497		
Leu Tyr Gly Ile Ala Glu Val Glu Ile Pro Asn Ile Gln Lys Gln Arg			
125	130	135	
aag cag ctt gca aga ttg gtg tta gac tgg gat tca gtc aga gcc agg	545		
Lys Gln Leu Ala Arg Leu Val Leu Asp Trp Asp Ser Val Arg Ala Arg			
140	145	150	
tgg aac caa gct cac aaa tcc tca gga acc aac ttt cag ggg ctt cca	593		
Trp Asn Gln Ala His Lys Ser Ser Gly Thr Asn Phe Gln Gly Leu Pro			
155	160	165	170
tca aaa ata gat act cta aag gaa gag atg gat gaa gct gga aat aaa	641		
Ser Lys Ile Asp Thr Leu Lys Glu Glu Met Asp Glu Ala Gly Asn Lys			
175	180	185	
gta gaa cag tgc aag gat caa ctt gca gca gac atg tac aac ttt atg	689		
Val Glu Gln Cys Lys Asp Gln Leu Ala Ala Asp Met Tyr Asn Phe Met			
190	195	200	

1241.22

gcc aaa gaa ggg gag tat ggc aaa ttc ttt gtt acg tta tta gaa gcc	737
Ala Lys Glu Gly Glu Tyr Gly Lys Phe Phe Val Thr Leu Leu Glu Ala	
205 210 215	
caa gca gat tac cat aga aaa gca tta gca gtc tta gaa aag acc ctc	785
Gln Ala Asp Tyr His Arg Lys Ala Leu Ala Val Leu Glu Lys Thr Leu	
220 225 230	
ccc gaa atg cga gcc cat caa gat aag tgg gcg gaa aaa cca gcc ttt	833
Pro Glu Met Arg Ala His Gln Asp Lys Trp Ala Glu Lys Pro Ala Phe	
235 240 245 250	
ggg act ccc cta gaa gaa cac ctg aag agg agc ggg cgc gag att gcg	881
Gly Thr Pro Leu Glu Glu His Leu Lys Arg Ser Gly Arg Glu Ile Ala	
255 260 265	
ctg ccc att gaa gcc tgt gtc atg ctg ctt ctg gag aca ggc atg aag	929
Leu Pro Ile Glu Ala Cys Val Met Leu Leu Leu Glu Thr Gly Met Lys	
270 275 280	
gag gag ggc ctt ttc cga att ggg gct ggg gcc tcc aag tta aag aag	977
Glu Glu Gly Leu Phe Arg Ile Gly Ala Gly Ala Ser Lys Leu Lys Lys	
285 290 295	
ctg aaa gct gct ttg gac tgt tct act tct cac ctg gat gag ttc tat	1025
Leu Lys Ala Ala Leu Asp Cys Ser Thr Ser His Leu Asp Glu Phe Tyr	
300 305 310	
tca gac ccc cat gct gta gca ggt gct tta aaa tcc tat tta cgg gaa	1073
Ser Asp Pro His Ala Val Ala Gly Ala Leu Lys Ser Tyr Leu Arg Glu	
315 320 325 330	
ttg cct gaa cct ttg atg act ttt aat ctg tat gaa gaa tgg aca caa	1121
Leu Pro Glu Pro Leu Met Thr Phe Asn Leu Tyr Glu Glu Trp Thr Gln	
335 340 345	
gtt gca agt gtg cag gat caa gac aaa aaa ctt caa gac ttg tgg aga	1169
Val Ala Ser Val Gln Asp Gln Asp Lys Lys Leu Gln Asp Leu Trp Arg	
350 355 360	
aca tgt cag aag ttg cca cca caa aat ttt gtt aac ttt aga tat ttg	1217
Thr Cys Gln Lys Leu Pro Pro Gln Asn Phe Val Asn Phe Arg Tyr Leu	

1241.22

365	370	375	
atc aag ttc ctt gca aag ctt gct cag acc agc gat gtg aat aaa atg			1265
Ile Lys Phe Leu Ala Lys Leu Ala Gln Thr Ser Asp Val Asn Lys Met			
380	385	390	
act ccc agc aac att gcg att gtg tta ggc cct aac ttg tta tgg gcc			1313
Thr Pro Ser Asn Ile Ala Ile Val Leu Gly Pro Asn Leu Leu Trp Ala			
395	400	405	410
aga aat gaa gga aca ctt gct gaa atg gca gca gcc aca tcc gtc cat			1361
Arg Asn Glu Gly Thr Leu Ala Glu Met Ala Ala Ala Thr Ser Val His			
415	420	425	
gtg gtt gca gtg att gaa ccc atc att cag cat gcc gac tgg ttc ttc			1409
Val Val Ala Val Ile Glu Pro Ile Ile Gln His Ala Asp Trp Phe Phe			
430	435	440	
cct gaa gag gtg gaa ttt aat gta tca gaa gca ttt gta cct ctc acc			1457
Pro Glu Glu Val Glu Phe Asn Val Ser Glu Ala Phe Val Pro Leu Thr			
445	450	455	
acc ccg agt tct aat cac tca ttc cac act gga aac gac tct gac tcg			1505
Thr Pro Ser Ser Asn His Ser Phe His Thr Gly Asn Asp Ser Asp Ser			
460	465	470	
ggg acc ctg gag agg aag cgg cct gct agc atg gcg gtg atg gaa gga			1553
Gly Thr Leu Glu Arg Lys Arg Pro Ala Ser Met Ala Val Met Glu Gly			
475	480	485	490
gac ttg gtg aag aag gaa agc ttt ggt gtg aag ctt atg gac ttc cag			1601
Asp Leu Val Lys Lys Glu Ser Phe Gly Val Lys Leu Met Asp Phe Gln			
495	500	505	
gcc cac cgg cgg ggt ggc act cta aat aga aag cac ata tcc ccc gct			1649
Ala His Arg Arg Gly Gly Thr Leu Asn Arg Lys His Ile Ser Pro Ala			
510	515	520	
ttc cag ccg cca ctt ccg ccc aca gat ggc agc acc gtg gtg ccc gct			1697
Phe Gln Pro Pro Leu Pro Pro Thr Asp Gly Ser Thr Val Val Pro Ala			
525	530	535	

1241.22

ggc cca gag ccc cct ccc cag agc tct agg gct gaa agc agc tct ggg	1745
Gly Pro Glu Pro Pro Pro Gln Ser Ser Arg Ala Glu Ser Ser Ser Gly	
540 545 550	
ggt ggg act gtc ccc tct tcc gcg ggc ata ctg gag cag ggg ccg agc	1793
Gly Gly Thr Val Pro Ser Ser Ala Gly Ile Leu Glu Gln Gly Pro Ser	
555 560 565 570	
cca ggc gac ggc agt cct ccc aaa ccg aag gac cct gta tct gca gct	1841
Pro Gly Asp Gly Ser Pro Pro Lys Pro Lys Asp Pro Val Ser Ala Ala	
575 580 585	
gtg cca gca cca ggg aga aac aac agt cag ata gca tct ggc caa aat	1889
Val Pro Ala Pro Gly Arg Asn Asn Ser Gln Ile Ala Ser Gly Gln Asn	
590 595 600	
cag ccc cag gca gct gct ggc tcc cac cag ctc tcc atg ggc caa cct	1937
Gln Pro Gln Ala Ala Ala Gly Ser His Gln Leu Ser Met Gly Gln Pro	
605 610 615	
cac aat gct gca ggg ccc agc ccg cat aca ctg cgc cga gct gtt aaa	1985
His Asn Ala Ala Gly Pro Ser Pro His Thr Leu Arg Arg Ala Val Lys	
620 625 630	
aaa ccc gct cca gca ccc ccg aaa ccg ggc aac cca cct cct ggc cac	2033
Lys Pro Ala Pro Ala Pro Pro Lys Pro Gly Asn Pro Pro Pro Gly His	
635 640 645 650	
ccc ggg ggc cag agt tct tca gga aca tct cag cat cca ccc agt ctg	2081
Pro Gly Gly Gln Ser Ser Ser Gly Thr Ser Gln His Pro Pro Ser Leu	
655 660 665	
tca cca aag cca ccc acc cga agc ccc tct cct ccc acc cag cac acg	2129
Ser Pro Lys Pro Pro Thr Arg Ser Pro Ser Pro Pro Thr Gln His Thr	
670 675 680	
ggc cag cct cca ggc cag ccc tcc gcc ccc tcc cag ctc tca gca ccc	2177
Gly Gln Pro Pro Gly Gln Pro Ser Ala Pro Ser Gln Leu Ser Ala Pro	
685 690 695	
cgg agg tac tcc agc agc ttg tct cca atc caa gct ccc aat cac cca	2225
Arg Arg Tyr Ser Ser Ser Leu Ser Pro Ile Gln Ala Pro Asn His Pro	

1241.22

700	705	710	
ccg ccg cag ccc cct acg cag gcc acg cca ctg atg cac acc aaa ccc			2273
Pro Pro Gln Pro Pro Thr Gln Ala Thr Pro Leu Met His Thr Lys Pro			
715	720	725	730
aat agc cag ggc cct ccc aac ccc atg gca ttg ccc agt gag cat gga			2321
Asn Ser Gln Gly Pro Pro Asn Pro Met Ala Leu Pro Ser Glu His Gly			
735	740	745	
ctt gag cag cca tct cac acc cct ccc cag act cca acg ccc ccc agt			2369
Leu Glu Gln Pro Ser His Thr Pro Pro Gln Thr Pro Thr Pro Pro Ser			
750	755	760	
act ccg ccc cta gga aaa cag aac ccc agt ctg cca gct cct cag acc			2417
Thr Pro Pro Leu Gly Lys Gln Asn Pro Ser Leu Pro Ala Pro Gln Thr			
765	770	775	
ctg gca ggg ggt aac cct gaa act gca cag cca cat gct gga acc tta			2465
Leu Ala Gly Gly Asn Pro Glu Thr Ala Gln Pro His Ala Gly Thr Leu			
780	785	790	
ccg aga ccg aga cca gta cca aag cca agg aac cgg ccc agc gtg ccc			2513
Pro Arg Pro Arg Pro Val Pro Lys Pro Arg Asn Arg Pro Ser Val Pro			
795	800	805	810
cca ccc ccc caa cct cct ggt gtc cac tca gct ggg gac agc agc ctc			2561
Pro Pro Pro Gln Pro Pro Gly Val His Ser Ala Gly Asp Ser Ser Leu			
815	820	825	
acc aac aca gca cca aca gct tcc aag ata gta aca gac tcc aat tcc			2609
Thr Asn Thr Ala Pro Thr Ala Ser Lys Ile Val Thr Asp Ser Asn Ser			
830	835	840	
agg gtt tca gaa ccg cat cgc agc atc ttt cct gaa atg cac tca gac			2657
Arg Val Ser Glu Pro His Arg Ser Ile Phe Pro Glu Met His Ser Asp			
845	850	855	
tca gcc agc aaa gac gtg cct ggc cgc atc ctg ctg gat ata gac aat			2705
Ser Ala Ser Lys Asp Val Pro Gly Arg Ile Leu Leu Asp Ile Asp Asn			
860	865	870	

1241.22

gat acc gag agc act gcc ctg tgaagaaagc cctttcccag ccctccacca 2756

Asp Thr Glu Ser Thr Ala Leu

875 880

cttccaccct ggcgagtgga gcaggggcag gcgaacctct ttctttgcag accgaacagt 2816

gaaaagcttt cagtggagga caaaggaggg cctcactgtg cgggacctgg ccttctgcac 2876

ggcccaagga gaacctggag gccaccacta aagctgaatg acctgtgtct tgaagaagtt 2936

ggctttcttt acatgggaag gaaatcatgc caaaaaaatc caaaacaaag aagtacctgg 2996

agtggagaga gtattcctgc tgaaacgcgc ataggaagct ttgtccctg ctgttaatgc 3056

gggcagcacc tacagcaact tggaatgagt aagaagcagt gcgttaacta tctatttaat 3116

aaaatgcgct cattatgcaa gtcgcctact ctctgctacc tggacgttca ttcttatgta 3176

ttaggagggg ggctgcgctc cttcagactt gctgcagaat cttttgtat catgtatgg 3236

ctgtgtctcc ccagtcccct cagaaccatg cccatggatg gtgactgctg gctctgtcac 3296

ctcatcaaac tggatgtgac ccatgccgcc tcgttgatt gtcggaatgt agacagaaat 3356

gtactgttct tttttttttt tttaaacaat gtaattgcta cttgataagg accgaacatt 3416

attctagttt catgtttaat ttgaattaaa tatattctgt ggtttatatg 3466

<210> 146

<211> 881

<212> PRT

<213> Homo sapiens

<400> 146

Met Lys Lys Gln Phe Asn Arg Met Lys Gln Leu Ala Asn Gln Thr Val

1 5 10 15

Gly Arg Ala Glu Lys Thr Glu Val Leu Ser Glu Asp Leu Leu Gln Ile

20 25 30

Glu Arg Arg Leu Asp Thr Val Arg Ser Ile Cys His His Ser His Lys

35 40 45

Arg Leu Val Ala Cys Phe Gln Gly Gln His Gly Thr Asp Ala Glu Arg

50 55 60

Arg His Lys Lys Leu Pro Leu Thr Ala Leu Ala Gln Asn Met Gln Glu

65 70 75 80

Ala Ser Thr Gln Leu Glu Asp Ser Leu Leu Gly Lys Met Leu Glu Thr

	85	1241.22	95
	90		
Cys Gly Asp Ala Glu Asn Gln Leu Ala Leu Glu Leu Ser Gln His Glu			
100	105	110	
Val Phe Val Glu Lys Glu Ile Val Asp Pro Leu Tyr Gly Ile Ala Glu			
115	120	125	
Val Glu Ile Pro Asn Ile Gln Lys Gln Arg Lys Gln Leu Ala Arg Leu			
130	135	140	
Val Leu Asp Trp Asp Ser Val Arg Ala Arg Trp Asn Gln Ala His Lys			
145	150	155	160
Ser Ser Gly Thr Asn Phe Gln Gly Leu Pro Ser Lys Ile Asp Thr Leu			
165	170	175	
Lys Glu Glu Met Asp Glu Ala Gly Asn Lys Val Glu Gln Cys Lys Asp			
180	185	190	
Gln Leu Ala Ala Asp Met Tyr Asn Phe Met Ala Lys Glu Gly Glu Tyr			
195	200	205	
Gly Lys Phe Phe Val Thr Leu Leu Glu Ala Gln Ala Asp Tyr His Arg			
210	215	220	
Lys Ala Leu Ala Val Leu Glu Lys Thr Leu Pro Glu Met Arg Ala His			
225	230	235	240
Gln Asp Lys Trp Ala Glu Lys Pro Ala Phe Gly Thr Pro Leu Glu Glu			
245	250	255	
His Leu Lys Arg Ser Gly Arg Glu Ile Ala Leu Pro Ile Glu Ala Cys			
260	265	270	
Val Met Leu Leu Leu Glu Thr Gly Met Lys Glu Glu Gly Leu Phe Arg			
275	280	285	
Ile Gly Ala Gly Ala Ser Lys Leu Lys Lys Leu Lys Ala Ala Leu Asp			
290	295	300	
Cys Ser Thr Ser His Leu Asp Glu Phe Tyr Ser Asp Pro His Ala Val			
305	310	315	320
Ala Gly Ala Leu Lys Ser Tyr Leu Arg Glu Leu Pro Glu Pro Leu Met			
325	330	335	
Thr Phe Asn Leu Tyr Glu Glu Trp Thr Gln Val Ala Ser Val Gln Asp			

1241.22

340	345	350
Gln Asp Lys Lys Leu Gln Asp Leu Trp Arg Thr Cys Gln Lys Leu Pro		
355	360	365
Pro Gln Asn Phe Val Asn Phe Arg Tyr Leu Ile Lys Phe Leu Ala Lys		
370	375	380
Leu Ala Gln Thr Ser Asp Val Asn Lys Met Thr Pro Ser Asn Ile Ala		
385	390	395
Ile Val Leu Gly Pro Asn Leu Leu Trp Ala Arg Asn Glu Gly Thr Leu		
405	410	415
Ala Glu Met Ala Ala Ala Thr Ser Val His Val Val Ala Val Ile Glu		
420	425	430
Pro Ile Ile Gln His Ala Asp Trp Phe Phe Pro Glu Glu Val Glu Phe		
435	440	445
Asn Val Ser Glu Ala Phe Val Pro Leu Thr Thr Pro Ser Ser Asn His		
450	455	460
Ser Phe His Thr Gly Asn Asp Ser Asp Ser Gly Thr Leu Glu Arg Lys		
465	470	475
Arg Pro Ala Ser Met Ala Val Met Glu Gly Asp Leu Val Lys Lys Glu		
485	490	495
Ser Phe Gly Val Lys Leu Met Asp Phe Gln Ala His Arg Arg Gly Gly		
500	505	510
Thr Leu Asn Arg Lys His Ile Ser Pro Ala Phe Gln Pro Pro Leu Pro		
515	520	525
Pro Thr Asp Gly Ser Thr Val Val Pro Ala Gly Pro Glu Pro Pro Pro		
530	535	540
Gln Ser Ser Arg Ala Glu Ser Ser Ser Gly Gly Gly Thr Val Pro Ser		
545	550	555
Ser Ala Gly Ile Leu Glu Gln Gly Pro Ser Pro Gly Asp Gly Ser Pro		
565	570	575
Pro Lys Pro Lys Asp Pro Val Ser Ala Ala Val Pro Ala Pro Gly Arg		
580	585	590

1241.22

Asn Asn Ser Gln Ile Ala Ser Gly Gln Asn Gln Pro Gln Ala Ala Ala
595 600 605
Gly Ser His Gln Leu Ser Met Gly Gln Pro His Asn Ala Ala Gly Pro
610 615 620
Ser Pro His Thr Leu Arg Arg Ala Val Lys Lys Pro Ala Pro Ala Pro
625 630 635 640
Pro Lys Pro Gly Asn Pro Pro Pro Gly His Pro Gly Gly Gln Ser Ser
645 650 655
Ser Gly Thr Ser Gln His Pro Pro Ser Leu Ser Pro Lys Pro Pro Thr
660 665 670
Arg Ser Pro Ser Pro Pro Thr Gln His Thr Gly Gln Pro Pro Gly Gln
675 680 685
Pro Ser Ala Pro Ser Gln Leu Ser Ala Pro Arg Arg Tyr Ser Ser Ser
690 695 700
Leu Ser Pro Ile Gln Ala Pro Asn His Pro Pro Pro Gln Pro Pro Thr
705 710 715 720
Gln Ala Thr Pro Leu Met His Thr Lys Pro Asn Ser Gln Gly Pro Pro
725 730 735
Asn Pro Met Ala Leu Pro Ser Glu His Gly Leu Glu Gln Pro Ser His
740 745 750
Thr Pro Pro Gln Thr Pro Thr Pro Pro Ser Thr Pro Pro Leu Gly Lys
755 760 765
Gln Asn Pro Ser Leu Pro Ala Pro Gln Thr Leu Ala Gly Gly Asn Pro
770 775 780
Glu Thr Ala Gln Pro His Ala Gly Thr Leu Pro Arg Pro Arg Pro Val
785 790 795 800
Pro Lys Pro Arg Asn Arg Pro Ser Val Pro Pro Pro Pro Gln Pro Pro
805 810 815
Gly Val His Ser Ala Gly Asp Ser Ser Leu Thr Asn Thr Ala Pro Thr
820 825 830
Ala Ser Lys Ile Val Thr Asp Ser Asn Ser Arg Val Ser Glu Pro His
835 840 845

1241.22

Arg Ser Ile Phe Pro Glu Met His Ser Asp Ser Ala Ser Lys Asp Val
850 855 860

Pro Gly Arg Ile Leu Leu Asp Ile Asp Asn Asp Thr Glu Ser Thr Ala
865 870 875 880
Leu

<210> 147

<211> 3021

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (140)..(1105)

<400> 147

gagctgccgc tgctgctctt gcttcagccg cagtcgccac tggctgcctg aggtgctctt 60
acagcctgtt ccaagtgtgg cttaatccgt ctccaccacc agatctttct ccgtggattc 120
ctctgctaag accgctgcc atg cca gtg acg gta acc cgc acc acc atc aca 172

Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr

1 5 10

acc acc acg acg tca tct tcg ggc ctg ggg tcc ccc atg atc gtg ggg 220
Thr Thr Thr Thr Ser Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly

15 20 25

tcc cct cgg gcc ctg aca cag ccc ctg ggt ctc ctt cgc ctg ctg cag 268
Ser Pro Arg Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln

30 35 40

ctg gtg tct acc tgc gtg gcc ttc tcg ctg gtg gct agc gtg ggc gcc 316
Leu Val Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala

45 50 55

tgg acg ggg tcc atg ggc aac tgg tcc atg ttc acc tgg tgc ttc tgc 364
Trp Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys

60 65 70 75

ttc tcc gtg acc ctg atc atc ctc atc gtg gag ctg tgc ggg ctc cag 412

1241.22

Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu Gln	
80 85 90	
gcc cgc ttc ccc ctg tct tgg cgc aac ttc ccc atc acc ttc gcc tgc	460
Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala Cys	
95 100 105	
tat gcg ggc ctc ttc tgc ctc tcg gcc tcc atc atc tac ccc acc acc	508
Tyr Ala Gly Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr Thr	
110 115 120	
tat gtc cag ttc ctg tcc cac ggc cgt tcg cgg gac cac gcc atc gcc	556
Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp His Ala Ile Ala	
125 130 135	
gcc acc ttc ttc tcc tgc atc gcg tgt gtg gct tac gcc acc gaa gtg	604
Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala Tyr Ala Thr Glu Val	
140 145 150 155	
gcc tgg acc cgg gcc cgg ccc ggc gag atc act ggc tat atg gcc acc	652
Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile Thr Gly Tyr Met Ala Thr	
160 165 170	
gta ccc ggg ctg ctg aag gtg ctg gag acc ttc gtt gcc tgc atc atc	700
Val Pro Gly Leu Leu Lys Val Leu Glu Thr Phe Val Ala Cys Ile Ile	
175 180 185	
ttc gcg ttc atc agc gac ccc aac ctg tac cag cac cag ccg gcc ctg	748
Phe Ala Phe Ile Ser Asp Pro Asn Leu Tyr Gln His Gln Pro Ala Leu	
190 195 200	
gag tgg tgc gtg gcg gtg tac gcc atc tgc ttc atc cta gcg gcc atc	796
Glu Trp Cys Val Ala Val Tyr Ala Ile Cys Phe Ile Leu Ala Ala Ile	
205 210 215	
gcc atc ctg ctg aac ctg ggg gag tgc acc aac gtg cta ccc atc ccc	844
Ala Ile Leu Leu Asn Leu Gly Glu Cys Thr Asn Val Leu Pro Ile Pro	
220 225 230 235	
ttc ccc agc ttc ctg tcg ggg ctg gcc ttg ctg tct gtc ctc ctc tat	892
Phe Pro Ser Phe Leu Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr	

1241.22

240	245	250	
gcc acc gcc ctt gtt ctc tgg ccc ctc tac cag ttc gat gag aag tat	940		
Ala Thr Ala Leu Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr			
255	260	265	
ggc ggc cag cct cgg cgc tcg aga gat gta agc tgc agc cgc agc cat	988		
Gly Gly Gln Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His			
270	275	280	
gcc tac tac gtg tgt gcc tgg gac cgc cga ctg gct gtg gcc atc ctg	1036		
Ala Tyr Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu			
285	290	295	
acg gcc atc aac cta ctg gcg tat gtg gct gac ctg gtg cac tct gcc	1084		
Thr Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala			
300	305	310	315
cac ctg gtt ttt gtc aag gtc taagactctc ccaagaggct cccgttcct	1135		
His Leu Val Phe Val Lys Val			

320

ctccaacctc ttgtttcttc ttgcccagat tttctttatg gactacttct ttcctccgcc	1195
tttctctgtg tttctctctc ctgtctcccc tccctccac cttttcttt cttcccaat	1255
tccttgcaact ctaaccagtt cttggatgca tcttcttctt tccctttcct cttgctgttt	1315
ccttctctgtg ttgttttgtt gccacatcc tgttttcacc cctgagctgt ttctcttttt	1375
cttttctttc tttttttttt ttttttaaga cggattctca ctctgtggcc caggctggag	1435
cgcagtgggtg cgatctcgac tctactgcaac cccgcctcc tgggttcaag cgattctcct	1495
gccccagcct cccaagtagc tgggaggaca ggtgtgagct gccgcacca gcctgtttct	1555
ctttttccac tcttcttttt tctcatctct tttctgggtt gcctgtcggc tttcttatct	1615
gcctgttttg caagcacctt ctctgtgtc cttgggagcc ctgagacttc tttctctcct	1675
tgccctccacc cacctccaaa ggtgctgagc tcacatccac accccttgca gccgtccatg	1735
ccacagcccc ccaaggggcc ccattgccaa agcatgcctg cccaccctcg ctgtgcctta	1795
gtcagtgtgt acgtgtgtgt gtgtgtgtgt ttgggggggtg ggggggtgggt agctggggat	1855
tggggcctct ttctcccagt ggaggaaggt gtgcagtgtta cttccccttt aaattaaaaa	1915
acatatatat atatatatat ggaggtcagt aatttccaat gggcgggagg cattaagcac	1975
cgaccctggg tccctaggcc ccgcctggca ctgagccttg ccagagattg gctccagaat	2035
ttttgccagg cttacagaac acccactgcc tagaggccat cttaaaggaa gcaggggctg	2095

1241.22

gatgcctttc atcccaacta ttctctgtgg tatgaaaaag aaaaaaaaaa aaaaagaagg 2155
agtcggggcc gggcgtggtg gctcacgcct gtaatcccag cactttggga gaccaagtca 2215
ggcaatcatc tgaagtcagg agttcaagac cagcctggcc aacatggtga aagcatgtct 2275
ctattaaaaa tacaaaaatt agccgggagc ggtggcgggc gcctgtaatc ccaggatattt 2335
ggggggactg agacaggaga atcccttcaa cccgggaggt ggagggtgca gtaagtcaag 2395
atggcaccac tgtgctccag cctgggggac agagcgagac tccatctcaa aaaaaaagg 2455
gaatcggacg aagaaccaca ggatgttgaa gacaactgtc tgaagtattt gtgagggaca 2515
gcgatgtggc cctctgtgtt aagaataacg tgtcctgctt tggcagagag aagaaaatag 2575
ccactgcccg ctttcaaggc aagatcgacc ttttctgttt tgttttgttt ttctttcttt 2635
ttcctggcca tgaggacaaa aattactgag tggcccttaa agagggaagt ttgttttcag 2695
ctgttctctt ttgcccgtag gtgggagggg ggggattgct gcgtcctagc tagaggaatg 2755
gctttgcttg aatgtgtagt gcacacgcac ggggtgttct gtgtgctagt tgcttcttgc 2815
tgctgcttcc tgcttgctct ggactcacat acataacgtg atatatatat atatatataa 2875
atgtataaat atatatattta ttttttttta aatccttgga gcttctgggt cctatcagtt 2935
cctgttgta atcgtagaac cgttgtccct tccccattc ccgtatccat catgttcttt 2995
ttcttttaaa tatcaatata aaagg 3021

<210> 148

<211> 322

<212> PRT

<213> Homo sapiens

<400> 148

Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr Thr Thr Thr Ser
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Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly Ser Pro Arg Ala Leu
20 25 30
Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val Ser Thr Cys
35 40 45
Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp Thr Gly Ser Met
50 55 60
Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys Phe Ser Val Thr Leu
65 70 75 80

1241.22

Ile Ile Leu Ile Val Glu Leu Cys Gly Leu Gln Ala Arg Phe Pro Leu
85 90 95
Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala Cys Tyr Ala Gly Leu Phe
100 105 110
Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr Thr Tyr Val Gln Phe Leu
115 120 125
Ser His Gly Arg Ser Arg Asp His Ala Ile Ala Ala Thr Phe Phe Ser
130 135 140
Cys Ile Ala Cys Val Ala Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala
145 150 155 160
Arg Pro Gly Glu Ile Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu
165 170 175
Lys Val Leu Glu Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser
180 185 190
Asp Pro Asn Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala
195 200 205
Val Tyr Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn
210 215 220
Leu Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu
225 230 235 240
Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu Val
245 250 255
Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln Pro Arg
260 265 270
Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr Tyr Val Cys
275 280 285
Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr Ala Ile Asn Leu
290 295 300
Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala His Leu Val Phe Val
305 310 315 320
Lys Val

1241.22

<210> 149

<211> 4409

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (39)..(2027)

<400> 149

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Met Ser Trp Leu Ser Ser

1

5

tcc cag gga gtg gta cta aca gcc tac cac ccc agc ggc aag gac cag 104

Ser Gln Gly Val Val Leu Thr Ala Tyr His Pro Ser Gly Lys Asp Gln

10

15

20

gcc gtc ggg aac agc cat gca aag gca ggg gag gaa gcc acc tcg agt 152

Ala Val Gly Asn Ser His Ala Lys Ala Gly Glu Glu Ala Thr Ser Ser

25

30

35

cgc aga tat ggc cag tac act atg aac cag gaa agc acc acc atc aaa 200

Arg Arg Tyr Gly Gln Tyr Thr Met Asn Gln Glu Ser Thr Thr Ile Lys

40

45

50

gtt atg gag aag cct cca ttt gat cga tca att tcc cag gat tct ttg 248

Val Met Glu Lys Pro Pro Phe Asp Arg Ser Ile Ser Gln Asp Ser Leu

55

60

65

70

gat gaa cta tct atg gaa gac tat tgg ata gaa cta gaa aac atc aag 296

Asp Glu Leu Ser Met Glu Asp Tyr Trp Ile Glu Leu Glu Asn Ile Lys

75

80

85

aaa tct agt gaa aac agc caa gaa gat caa gag gtg gtt gtt gtc aaa 344

Lys Ser Ser Glu Asn Ser Gln Glu Asp Gln Glu Val Val Val Val Lys

90

95

100

gag cct gat gag gga gaa ttg gaa gaa gag tgg ctt aaa gag gcc ggt 392

Glu Pro Asp Glu Gly Glu Leu Glu Glu Glu Trp Leu Lys Glu Ala Gly

1241.22

105	110	115	
tta tcc aat ctc ttc gga gag tct gct gga gat cca cag gaa agc att			440
Leu Ser Asn Leu Phe Gly Glu Ser Ala Gly Asp Pro Gln Glu Ser Ile			
120	125	130	
gtg ttt tta tca aca ttg acg cgg acc cag gca gca gca gtt cag aag			488
Val Phe Leu Ser Thr Leu Thr Arg Thr Gln Ala Ala Ala Val Gln Lys			
135	140	145	150
cga gta gag acg gtc tcc cag acc ttg agg aaa aaa aac aaa cag tac			536
Arg Val Glu Thr Val Ser Gln Thr Leu Arg Lys Lys Asn Lys Gln Tyr			
155	160	165	
cag att cct gac gtc aga gac ata ttt gct caa cag aga gaa tca aaa			584
Gln Ile Pro Asp Val Arg Asp Ile Phe Ala Gln Gln Arg Glu Ser Lys			
170	175	180	
gaa aca gct cca ggt ggc act gaa tcg cag tca ctt aga aca aat gaa			632
Glu Thr Ala Pro Gly Gly Thr Glu Ser Gln Ser Leu Arg Thr Asn Glu			
185	190	195	
aac aaa tac caa gga aga gat gac gag gca tct aac ctt gtt ggt gaa			680
Asn Lys Tyr Gln Gly Arg Asp Asp Glu Ala Ser Asn Leu Val Gly Glu			
200	205	210	
gag aag ctg atc cca cct gag gag acg cct gcc cct gaa aca gac atc			728
Glu Lys Leu Ile Pro Pro Glu Glu Thr Pro Ala Pro Glu Thr Asp Ile			
215	220	225	230
aac ctg gag gta tca ttt gcc gag caa gca ctc aat cag aaa gag agc			776
Asn Leu Glu Val Ser Phe Ala Glu Gln Ala Leu Asn Gln Lys Glu Ser			
235	240	245	
tcc aag gag aaa atc cag aag agc aaa ggc gat gat gcc aca tta cct			824
Ser Lys Glu Lys Ile Gln Lys Ser Lys Gly Asp Asp Ala Thr Leu Pro			
250	255	260	
agt ttc aga ttg cca aaa gac aaa acg ggt acc aca agg att ggt gac			872
Ser Phe Arg Leu Pro Lys Asp Lys Thr Gly Thr Thr Arg Ile Gly Asp			
265	270	275	
ctc gca ccc cag gac atg aag aaa gtt tgc cat tta gcc cta att gag			920

1241.22

Leu Ala Pro Gln Asp Met Lys Lys Val Cys His Leu Ala Leu Ile Glu	
280 285 290	
ctg act gcc ctc tat gat gta ttg ggt att gag ctg aaa caa caa aaa	968
Leu Thr Ala Leu Tyr Asp Val Leu Gly Ile Glu Leu Lys Gln Gln Lys	
295 300 305 310	
gct gtg aaa atc aaa aca aaa gat tct ggt ctt ttt tgc gtt cca ttg	1016
Ala Val Lys Ile Lys Thr Lys Asp Ser Gly Leu Phe Cys Val Pro Leu	
315 320 325	
aca gcg cta tta gaa caa gat cag agg aaa gta cca gga atg cga ata	1064
Thr Ala Leu Leu Glu Gln Asp Gln Arg Lys Val Pro Gly Met Arg Ile	
330 335 340	
ccc ttg atc ttt caa aaa ctg att tct cga att gaa gag aga ggt ttg	1112
Pro Leu Ile Phe Gln Lys Leu Ile Ser Arg Ile Glu Glu Arg Gly Leu	
345 350 355	
gaa aca gaa ggc ctc tta cgg atc cct gga gct gcc att aga atc aag	1160
Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly Ala Ala Ile Arg Ile Lys	
360 365 370	
aat ctt tgc caa gaa cta gaa gca aag ttt tat gaa ggg act ttt aat	1208
Asn Leu Cys Gln Glu Leu Glu Ala Lys Phe Tyr Glu Gly Thr Phe Asn	
375 380 385 390	
tgg gaa agt gtc aaa cag cat gat gcc gcc agc ctg ctg aag ctc ttc	1256
Trp Glu Ser Val Lys Gln His Asp Ala Ala Ser Leu Leu Lys Leu Phe	
395 400 405	
att cgg gag ttg ccc cag cca ctg ctc agt gtg gag tat ctc aaa gcc	1304
Ile Arg Glu Leu Pro Gln Pro Leu Leu Ser Val Glu Tyr Leu Lys Ala	
410 415 420	
ttt cag gct gtc cag aat ctt cca acc aag aag cag caa cta cag gct	1352
Phe Gln Ala Val Gln Asn Leu Pro Thr Lys Lys Gln Gln Leu Gln Ala	
425 430 435	
ttg aac ctt ctt ggc atc ctc cta cct gat gca aac agg gac aca ctg	1400
Leu Asn Leu Leu Gly Ile Leu Leu Pro Asp Ala Asn Arg Asp Thr Leu	

1241.22

440	445	450	
aag gcc ctt ctt gaa ttt ctc caa aga gta ata gat aat aaa gaa aaa			1448
Lys Ala Leu Leu Glu Phe Leu Gln Arg Val Ile Asp Asn Lys Glu Lys			
455	460	465	470
aat aaa atg aca gtc atg aat gta gca atg gtc atg gcc ccg aat ctc			1496
Asn Lys Met Thr Val Met Asn Val Ala Met Val Met Ala Pro Asn Leu			
	475	480	485
ttt atg tgt cat gca ttg gga ttg aag tcc agt gaa cag cga gaa ttt			1544
Phe Met Cys His Ala Leu Gly Leu Lys Ser Ser Glu Gln Arg Glu Phe			
	490	495	500
gta atg gca gct ggg aca gca aat acc atg cac tta ttg att aag tac			1592
Val Met Ala Ala Gly Thr Ala Asn Thr Met His Leu Leu Ile Lys Tyr			
	505	510	515
caa aaa ctt ctg tgg aca att ccc aag ttt att gta aac caa gtg agg			1640
Gln Lys Leu Leu Trp Thr Ile Pro Lys Phe Ile Val Asn Gln Val Arg			
	520	525	530
aag caa aac acg gaa aat cat aaa aag gat aaa aga gcc atg aag aaa			1688
Lys Gln Asn Thr Glu Asn His Lys Lys Asp Lys Arg Ala Met Lys Lys			
535	540	545	550
ttg ctg aag aaa atg gct tat gac cga gaa aaa tat gaa aag caa gat			1736
Leu Leu Lys Lys Met Ala Tyr Asp Arg Glu Lys Tyr Glu Lys Gln Asp			
	555	560	565
aag agt aca aat gat gct gac gtt cct cag gga gtg att cga gtg caa			1784
Lys Ser Thr Asn Asp Ala Asp Val Pro Gln Gly Val Ile Arg Val Gln			
	570	575	580
gct ccc cat ctt tcg aaa gtt tcc atg gca ata cag cta act gaa gaa			1832
Ala Pro His Leu Ser Lys Val Ser Met Ala Ile Gln Leu Thr Glu Glu			
	585	590	595
cta aaa gcc agt gat gta ctt gcc agg ttt ctc agc caa gaa agt ggg			1880
Leu Lys Ala Ser Asp Val Leu Ala Arg Phe Leu Ser Gln Glu Ser Gly			
	600	605	610
gtt gcc cag act ctc aag aaa gga gaa gtt ttt ttg tat gaa att gga			1928

1241.22

Val Ala Gln Thr Leu Lys Lys Gly Glu Val Phe Leu Tyr Glu Ile Gly
615 620 625 630
gga aat att ggg gaa cgc tgc ctt gat gat gac act tac atg aag gat 1976
Gly Asn Ile Gly Glu Arg Cys Leu Asp Asp Asp Thr Tyr Met Lys Asp
635 640 645
tta tat cag ctt aac cca aat gct gag tgg gtt ata aag tca aag cca 2024
Leu Tyr Gln Leu Asn Pro Asn Ala Glu Trp Val Ile Lys Ser Lys Pro
650 655 660
ttg tagaagactt aacaagctgc agataacccat gtggacttct gtcataattc 2077
Leu
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gatgtctcta atgaaggggg ggaatgctgt taatgagaac agtcataaat ttttagcata 3337

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taattacaag aacagcctgt ggatatgatc acttaaataga ttttgtggtg attcgtgcc 3397
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<211> 663

<212> PRT

<213> Homo sapiens

<400> 150

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Pro Ser Gly Lys Asp Gln Ala Val Gly Asn Ser His Ala Lys Ala Gly
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Glu Glu Ala Thr Ser Ser Arg Arg Tyr Gly Gln Tyr Thr Met Asn Gln
35 40 45
Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro Pro Phe Asp Arg Ser
50 55 60

1241.22

Ile	Ser	Gln	Asp	Ser	Leu	Asp	Glu	Leu	Ser	Met	Glu	Asp	Tyr	Trp	Ile
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Glu	Leu	Glu	Asn	Ile	Lys	Lys	Ser	Ser	Glu	Asn	Ser	Gln	Glu	Asp	Gln
				85						90					95
Glu	Val	Val	Val	Val	Lys	Glu	Pro	Asp	Glu	Gly	Glu	Leu	Glu	Glu	Glu
				100					105						110
Trp	Leu	Lys	Glu	Ala	Gly	Leu	Ser	Asn	Leu	Phe	Gly	Glu	Ser	Ala	Gly
		115						120						125	
Asp	Pro	Gln	Glu	Ser	Ile	Val	Phe	Leu	Ser	Thr	Leu	Thr	Arg	Thr	Gln
		130					135						140		
Ala	Ala	Ala	Val	Gln	Lys	Arg	Val	Glu	Thr	Val	Ser	Gln	Thr	Leu	Arg
145					150						155				160
Lys	Lys	Asn	Lys	Gln	Tyr	Gln	Ile	Pro	Asp	Val	Arg	Asp	Ile	Phe	Ala
				165						170					175
Gln	Gln	Arg	Glu	Ser	Lys	Glu	Thr	Ala	Pro	Gly	Gly	Thr	Glu	Ser	Gln
				180						185					190
Ser	Leu	Arg	Thr	Asn	Glu	Asn	Lys	Tyr	Gln	Gly	Arg	Asp	Asp	Glu	Ala
		195						200						205	
Ser	Asn	Leu	Val	Gly	Glu	Glu	Lys	Leu	Ile	Pro	Pro	Glu	Glu	Thr	Pro
		210					215							220	
Ala	Pro	Glu	Thr	Asp	Ile	Asn	Leu	Glu	Val	Ser	Phe	Ala	Glu	Gln	Ala
225						230						235			240
Leu	Asn	Gln	Lys	Glu	Ser	Ser	Lys	Glu	Lys	Ile	Gln	Lys	Ser	Lys	Gly
				245						250					255
Asp	Asp	Ala	Thr	Leu	Pro	Ser	Phe	Arg	Leu	Pro	Lys	Asp	Lys	Thr	Gly
			260						265						270
Thr	Thr	Arg	Ile	Gly	Asp	Leu	Ala	Pro	Gln	Asp	Met	Lys	Lys	Val	Cys
			275					280						285	
His	Leu	Ala	Leu	Ile	Glu	Leu	Thr	Ala	Leu	Tyr	Asp	Val	Leu	Gly	Ile
		290						295							300
Glu	Leu	Lys	Gln	Gln	Lys	Ala	Val	Lys	Ile	Lys	Thr	Lys	Asp	Ser	Gly
305						310					315				320

1241.22

Leu Phe Cys Val Pro Leu Thr Ala Leu Leu Glu Gln Asp Gln Arg Lys
325 330 335
Val Pro Gly Met Arg Ile Pro Leu Ile Phe Gln Lys Leu Ile Ser Arg
340 345 350
Ile Glu Glu Arg Gly Leu Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly
355 360 365
Ala Ala Ile Arg Ile Lys Asn Leu Cys Gln Glu Leu Glu Ala Lys Phe
370 375 380
Tyr Glu Gly Thr Phe Asn Trp Glu Ser Val Lys Gln His Asp Ala Ala
385 390 395 400
Ser Leu Leu Lys Leu Phe Ile Arg Glu Leu Pro Gln Pro Leu Leu Ser
405 410 415
Val Glu Tyr Leu Lys Ala Phe Gln Ala Val Gln Asn Leu Pro Thr Lys
420 425 430
Lys Gln Gln Leu Gln Ala Leu Asn Leu Leu Gly Ile Leu Leu Pro Asp
435 440 445
Ala Asn Arg Asp Thr Leu Lys Ala Leu Leu Glu Phe Leu Gln Arg Val
450 455 460
Ile Asp Asn Lys Glu Lys Asn Lys Met Thr Val Met Asn Val Ala Met
465 470 475 480
Val Met Ala Pro Asn Leu Phe Met Cys His Ala Leu Gly Leu Lys Ser
485 490 495
Ser Glu Gln Arg Glu Phe Val Met Ala Ala Gly Thr Ala Asn Thr Met
500 505 510
His Leu Leu Ile Lys Tyr Gln Lys Leu Leu Trp Thr Ile Pro Lys Phe
515 520 525
Ile Val Asn Gln Val Arg Lys Gln Asn Thr Glu Asn His Lys Lys Asp
530 535 540
Lys Arg Ala Met Lys Lys Leu Leu Lys Lys Met Ala Tyr Asp Arg Glu
545 550 555 560
Lys Tyr Glu Lys Gln Asp Lys Ser Thr Asn Asp Ala Asp Val Pro Gln

1241.22

565 570 575

Gly Val Ile Arg Val Gln Ala Pro His Leu Ser Lys Val Ser Met Ala

580 585 590

Ile Gln Leu Thr Glu Glu Leu Lys Ala Ser Asp Val Leu Ala Arg Phe

595 600 605

Leu Ser Gln Glu Ser Gly Val Ala Gln Thr Leu Lys Lys Gly Glu Val

610 615 620

Phe Leu Tyr Glu Ile Gly Gly Asn Ile Gly Glu Arg Cys Leu Asp Asp

625 630 635 640

Asp Thr Tyr Met Lys Asp Leu Tyr Gln Leu Asn Pro Asn Ala Glu Trp

645 650 655

Val Ile Lys Ser Lys Pro Leu

660

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<211> 4490

<212> DNA

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<220>

<221> CDS

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<400> 151

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aac tca aca ctg agt gac agc ggt atg att gat aat ctt cca gac agc	95
Asn Ser Thr Leu Ser Asp Ser Gly Met Ile Asp Asn Leu Pro Asp Ser	
20 25 30	
cca gac gag gta gcc aag gag ctg gag ctg ctc ggg gga tgg aca gat	143
Pro Asp Glu Val Ala Lys Glu Leu Glu Leu Leu Gly Gly Trp Thr Asp	
35 40 45	
gac aaa aaa gta cca ggc aga atg tac agt aat aac cct ttc tgg aat	191

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Asp	Lys	Lys	Val	Pro	Gly	Arg	Met	Tyr	Ser	Asn	Asn	Pro	Phe	Trp	Asn	
50				55				60								
ggg	gtc	cag	acc	aat	cca	ttt	ctg	aat	ggg	aac	gtg	ccc	gtc	atg	ccc	239
Gly	Val	Gln	Thr	Asn	Pro	Phe	Leu	Asn	Gly	Asn	Val	Pro	Val	Met	Pro	
65				70				75								
agc	ctg	gat	gag	ctg	aat	ccc	aaa	agt	act	gtg	gat	ttg	ctc	ctt	ttt	287
Ser	Leu	Asp	Glu	Leu	Asn	Pro	Lys	Ser	Thr	Val	Asp	Leu	Leu	Leu	Phe	
80				85				90				95				
gac	gca	ggt	aca	tcc	tcc	ttc	acc	gaa	tcc	agc	tca	gcc	acc	acg	aat	335
Asp	Ala	Gly	Thr	Ser	Ser	Phe	Thr	Glu	Ser	Ser	Ser	Ala	Thr	Thr	Asn	
100				105				110								
agc	act	ggc	aac	atc	ttc	gat	gag	ctt	cca	gtc	aca	aac	ggg	ctc	cac	383
Ser	Thr	Gly	Asn	Ile	Phe	Asp	Glu	Leu	Pro	Val	Thr	Asn	Gly	Leu	His	
115				120				125								
gca	gag	ccg	ccg	gtc	agg	cgg	gac	aac	ccc	ttc	ttc	aga	agc	aag	cgc	431
Ala	Glu	Pro	Pro	Val	Arg	Arg	Asp	Asn	Pro	Phe	Phe	Arg	Ser	Lys	Arg	
130				135				140								
tcc	tac	agt	ctc	tcg	gaa	ctc	tcc	gtc	ctc	caa	gcc	aag	tcc	gac	gct	479
Ser	Tyr	Ser	Leu	Ser	Glu	Leu	Ser	Val	Leu	Gln	Ala	Lys	Ser	Asp	Ala	
145				150				155								
ccc	aca	tcg	tcg	agt	ttc	ttc	acc	ggc	ttg	aaa	tca	cct	gcc	ccc	gag	527
Pro	Thr	Ser	Ser	Ser	Phe	Phe	Thr	Gly	Leu	Lys	Ser	Pro	Ala	Pro	Glu	
160				165				170				175				
caa	ttt	cag	agc	cgg	gag	gat	ttt	cga	act	gcc	tgg	cta	aac	cac	agg	575
Gln	Phe	Gln	Ser	Arg	Glu	Asp	Phe	Arg	Thr	Ala	Trp	Leu	Asn	His	Arg	
180				185				190								
aag	ctg	gcc	cgg	tct	tgc	cac	gac	ctg	gac	ttg	ctt	ggc	caa	agc	cct	623
Lys	Leu	Ala	Arg	Ser	Cys	His	Asp	Leu	Asp	Leu	Leu	Gly	Gln	Ser	Pro	
195				200				205								
ggg	tgg	ggc	cag	acc	caa	gcc	gtg	gag	aca	aac	atc	gtg	tgc	aag	ctg	671
Gly	Trp	Gly	Gln	Thr	Gln	Ala	Val	Glu	Thr	Asn	Ile	Val	Cys	Lys	Leu	
210				215				220								

1241.22

gat agc tcc ggg ggt gct gtc cag ctt cct gac acc agc atc agc atc	719
Asp Ser Ser Gly Gly Ala Val Gln Leu Pro Asp Thr Ser Ile Ser Ile	
225 230 235	
cac gtg ccc gag ggc cac gtc gcc cct ggg gag acc cag cag atc tcc	767
His Val Pro Glu Gly His Val Ala Pro Gly Glu Thr Gln Gln Ile Ser	
240 245 250 255	
atg aaa gcc ctg ctg gac ccc ccg ctg gag ctc aac agt gac agg tcc	815
Met Lys Ala Leu Leu Asp Pro Pro Leu Glu Leu Asn Ser Asp Arg Ser	
260 265 270	
tgc agc atc agc cct gtg ctg gag gtc aag ctg agc aac ctg gag gtg	863
Cys Ser Ile Ser Pro Val Leu Glu Val Lys Leu Ser Asn Leu Glu Val	
275 280 285	
aaa acc tct atc atc ttg gag atg aaa gtg tca gcc gag ata aaa aat	911
Lys Thr Ser Ile Ile Leu Glu Met Lys Val Ser Ala Glu Ile Lys Asn	
290 295 300	
gac ctt ttt agc aaa agc aca gtg ggc ctc cag tgc ctg agg agc gac	959
Asp Leu Phe Ser Lys Ser Thr Val Gly Leu Gln Cys Leu Arg Ser Asp	
305 310 315	
tcg aag gaa ggg cca tat gtc tcc gtc ccg ctc aac tgc agc tgt ggg	1007
Ser Lys Glu Gly Pro Tyr Val Ser Val Pro Leu Asn Cys Ser Cys Gly	
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Asp Thr Val Gln Ala Gln Leu His Asn Leu Glu Pro Cys Met Tyr Val	
340 345 350	
gct gtc gtg gcc cat ggc cca agc atc ctc tac cct tcc acc gtg tgg	1103
Ala Val Val Ala His Gly Pro Ser Ile Leu Tyr Pro Ser Thr Val Trp	
355 360 365	
gac ttc atc aat aaa aaa gtc aca gtg ggt ctc tac ggc cct aaa cac	1151
Asp Phe Ile Asn Lys Lys Val Thr Val Gly Leu Tyr Gly Pro Lys His	
370 375 380	
atc cac cca tcc ttc aag acg gta gtg acc att ttt ggg cat gac tgt	1199

1241.22

Ile His Pro Ser Phe Lys Thr Val Val Thr Ile Phe Gly His Asp Cys	
385	390 395
gcc cca aag acg ctc ctg gtc agc gag gtc aca cgc cag gca ccc aac	1247
Ala Pro Lys Thr Leu Leu Val Ser Glu Val Thr Arg Gln Ala Pro Asn	
400	405 410 415
cct gcc ccg gtg gcc ctg cag ctg tgg ggg aag cac cag ttc gtt ttg	1295
Pro Ala Pro Val Ala Leu Gln Leu Trp Gly Lys His Gln Phe Val Leu	
420	425 430
tcc agg ccc cag gat ctc aag gtc tgt atg ttt tcc aat atg acg aat	1343
Ser Arg Pro Gln Asp Leu Lys Val Cys Met Phe Ser Asn Met Thr Asn	
435	440 445
tac gag gtc aaa gcc agc gag cag gcc aaa gtg gtg cga gga ttc cag	1391
Tyr Glu Val Lys Ala Ser Glu Gln Ala Lys Val Val Arg Gly Phe Gln	
450	455 460
ctg aag ctg ggc aag gtg agc cgc ctg atc ttc ccc atc acc tcc cag	1439
Leu Lys Leu Gly Lys Val Ser Arg Leu Ile Phe Pro Ile Thr Ser Gln	
465	470 475
aac ccc aac gag ctc tct gac ttc acg ctg cgg gtt cag gtg aag gac	1487
Asn Pro Asn Glu Leu Ser Asp Phe Thr Leu Arg Val Gln Val Lys Asp	
480	485 490 495
gac cag gag gcc atc ctc acc cag ttt tgt gtc cag act cct cag cca	1535
Asp Gln Glu Ala Ile Leu Thr Gln Phe Cys Val Gln Thr Pro Gln Pro	
500	505 510
ccc cct aaa agt gcc atc aag cct tcc ggg caa agg agg ttt ctc aag	1583
Pro Pro Lys Ser Ala Ile Lys Pro Ser Gly Gln Arg Arg Phe Leu Lys	
515	520 525
aag aac gaa gtc ggg aaa atc atc ctg tcc ccg ttt gcc acc act aca	1631
Lys Asn Glu Val Gly Lys Ile Ile Leu Ser Pro Phe Ala Thr Thr Thr	
530	535 540
aag tac ccg act ttc cag gac cgc ccg gtg tcc agc ctc aag ttt ggt	1679
Lys Tyr Pro Thr Phe Gln Asp Arg Pro Val Ser Ser Leu Lys Phe Gly	
545	550 555

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aag	ttg	ctc	aag	act	gtg	gtg	cgg	cag	aac	aag	aac	cac	tac	ctg	ctg	1727
Lys	Leu	Leu	Lys	Thr	Val	Val	Arg	Gln	Asn	Lys	Asn	His	Tyr	Leu	Leu	
560			565			570			575							
gag	tac	aag	aag	ggc	gac	ggg	atc	gcc	ctg	ctc	agc	gag	gag	cgg	gtc	1775
Glu	Tyr	Lys	Lys	Gly	Asp	Gly	Ile	Ala	Leu	Leu	Ser	Glu	Glu	Arg	Val	
580			585			590										
agg	ctc	cgg	ggc	cag	ctg	tgg	acc	aag	gag	tgg	tac	atc	ggc	tac	tac	1823
Arg	Leu	Arg	Gly	Gln	Leu	Trp	Thr	Lys	Glu	Trp	Tyr	Ile	Gly	Tyr	Tyr	
595			600			605										
cag	ggc	agg	gtg	ggc	ctc	gtg	cac	acc	aag	aac	gtg	ctg	gtg	gtc	ggc	1871
Gln	Gly	Arg	Val	Gly	Leu	Val	His	Thr	Lys	Asn	Val	Leu	Val	Val	Gly	
610			615			620										
agg	gcc	cgg	ccc	agc	ctg	tgc	tcg	ggc	ccc	gag	ctg	agc	acc	tcg	gtg	1919
Arg	Ala	Arg	Pro	Ser	Leu	Cys	Ser	Gly	Pro	Glu	Leu	Ser	Thr	Ser	Val	
625			630			635										
ctg	ctg	gag	cag	atc	ctg	cgg	ccc	tgc	aaa	ttc	ctc	acg	tac	atc	tat	1967
Leu	Leu	Glu	Gln	Ile	Leu	Arg	Pro	Cys	Lys	Phe	Leu	Thr	Tyr	Ile	Tyr	
640			645			650			655							
gcc	tcc	gtg	agg	acc	ctg	ctc	atg	gag	aac	atc	agc	agc	tgg	cgc	tcc	2015
Ala	Ser	Val	Arg	Thr	Leu	Leu	Met	Glu	Asn	Ile	Ser	Ser	Trp	Arg	Ser	
660			665			670										
ttc	gct	gac	gcc	ctg	ggc	tac	gtg	aac	ctg	ccg	ctc	acc	ttt	ttc	tgc	2063
Phe	Ala	Asp	Ala	Leu	Gly	Tyr	Val	Asn	Leu	Pro	Leu	Thr	Phe	Phe	Cys	
675			680			685										
cgg	gca	gag	ctg	gat	agt	gag	ccc	gag	cgg	gtg	gcg	tcc	gtc	ctg	gaa	2111
Arg	Ala	Glu	Leu	Asp	Ser	Glu	Pro	Glu	Arg	Val	Ala	Ser	Val	Leu	Glu	
690			695			700										
aag	ctg	aag	gag	gac	tgt	aac	aac	act	gag	aac	aaa	gaa	cgg	aag	tcc	2159
Lys	Leu	Lys	Glu	Asp	Cys	Asn	Asn	Thr	Glu	Asn	Lys	Glu	Arg	Lys	Ser	
705			710			715										
ttc	cag	aag	gag	ctt	gtg	atg	gcc	cta	ctg	aag	atg	gac	tgc	cag	ggc	2207

1241.22

Phe Gln Lys Glu Leu Val Met Ala Leu Leu Lys Met Asp Cys Gln Gly
720 725 730 735
ctg gtg gtc aga ctc atc cag gac ttt gtg ctc ctg acc acg gct gta 2255
Leu Val Val Arg Leu Ile Gln Asp Phe Val Leu Leu Thr Thr Ala Val
740 745 750
gag gtg gcc cag cgc tgg cgg gag ctg gct gag aag ctg gcc aag gtc 2303
Glu Val Ala Gln Arg Trp Arg Glu Leu Ala Glu Lys Leu Ala Lys Val
755 760 765
tcc aag cag cag atg gac gcc tac gag tct ccc cac cgg gac agg aac 2351
Ser Lys Gln Gln Met Asp Ala Tyr Glu Ser Pro His Arg Asp Arg Asn
770 775 780
ggg gtt gtg gac agc gag gcc atg tgg aag cct gcg tat gac ttc tta 2399
Gly Val Val Asp Ser Glu Ala Met Trp Lys Pro Ala Tyr Asp Phe Leu
785 790 795
ctc acc tgg agc cat cag atc ggg gac agc tac cgg gat gtc atc cag 2447
Leu Thr Trp Ser His Gln Ile Gly Asp Ser Tyr Arg Asp Val Ile Gln
800 805 810 815
gag ctg cac ctg ggc ctg gac aag atg aaa aac ccc atc acc aag cgc 2495
Glu Leu His Leu Gly Leu Asp Lys Met Lys Asn Pro Ile Thr Lys Arg
820 825 830
tgg aag cac ctc act ggg act ctg atc ttg gtg aac tcc ctg gac gtt 2543
Trp Lys His Leu Thr Gly Thr Leu Ile Leu Val Asn Ser Leu Asp Val
835 840 845
ctg aga gca gcc gcc ttc agc cct gcg gac cag gac gac ttc gtg att 2591
Leu Arg Ala Ala Ala Phe Ser Pro Ala Asp Gln Asp Asp Phe Val Ile
850 855 860
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 tagaatatgt gaatctttgg tgagcttcag tgggcagagt gaagtcccg attagcattt 3311
 aggtgccctg agctgtttct gccaatagat tagaaagcag ccatgagttg acagtcttta 3371
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 tatgctgatg tgcagaggtg ccagctgcca ttgccaac tctgcatttc atttcatcta 3671
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<210> 152

<211> 863

<212> PRT

<213> Homo sapiens

<400> 152

1241.22

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Ser	Thr	Leu	Ser	Asp	Ser	Gly	Met	Ile	Asp	Asn	Leu	Pro	Asp	Ser	Pro
			20					25					30		
Asp	Glu	Val	Ala	Lys	Glu	Leu	Glu	Leu	Gly	Gly	Trp	Thr	Asp	Asp	
		35					40					45			
Lys	Lys	Val	Pro	Gly	Arg	Met	Tyr	Ser	Asn	Asn	Pro	Phe	Trp	Asn	Gly
	50					55					60				
Val	Gln	Thr	Asn	Pro	Phe	Leu	Asn	Gly	Asn	Val	Pro	Val	Met	Pro	Ser
65					70					75					80
Leu	Asp	Glu	Leu	Asn	Pro	Lys	Ser	Thr	Val	Asp	Leu	Leu	Leu	Phe	Asp
				85						90				95	
Ala	Gly	Thr	Ser	Ser	Phe	Thr	Glu	Ser	Ser	Ser	Ala	Thr	Thr	Asn	Ser
		100						105					110		
Thr	Gly	Asn	Ile	Phe	Asp	Glu	Leu	Pro	Val	Thr	Asn	Gly	Leu	His	Ala
	115						120					125			
Glu	Pro	Pro	Val	Arg	Arg	Asp	Asn	Pro	Phe	Phe	Arg	Ser	Lys	Arg	Ser
	130					135					140				
Tyr	Ser	Leu	Ser	Glu	Leu	Ser	Val	Leu	Gln	Ala	Lys	Ser	Asp	Ala	Pro
145					150					155					160
Thr	Ser	Ser	Ser	Phe	Phe	Thr	Gly	Leu	Lys	Ser	Pro	Ala	Pro	Glu	Gln
				165						170				175	
Phe	Gln	Ser	Arg	Glu	Asp	Phe	Arg	Thr	Ala	Trp	Leu	Asn	His	Arg	Lys
		180					185						190		
Leu	Ala	Arg	Ser	Cys	His	Asp	Leu	Asp	Leu	Leu	Gly	Gln	Ser	Pro	Gly
	195						200					205			
Trp	Gly	Gln	Thr	Gln	Ala	Val	Glu	Thr	Asn	Ile	Val	Cys	Lys	Leu	Asp
	210					215					220				
Ser	Ser	Gly	Gly	Ala	Val	Gln	Leu	Pro	Asp	Thr	Ser	Ile	Ser	Ile	His
225					230					235					240
Val	Pro	Glu	Gly	His	Val	Ala	Pro	Gly	Glu	Thr	Gln	Gln	Ile	Ser	Met

1241.22

245	250	255
Lys Ala Leu Leu Asp Pro Pro Leu Glu Leu Asn Ser Asp Arg Ser Cys		
260	265	270
Ser Ile Ser Pro Val Leu Glu Val Lys Leu Ser Asn Leu Glu Val Lys		
275	280	285
Thr Ser Ile Ile Leu Glu Met Lys Val Ser Ala Glu Ile Lys Asn Asp		
290	295	300
Leu Phe Ser Lys Ser Thr Val Gly Leu Gln Cys Leu Arg Ser Asp Ser		
305	310	315
Lys Glu Gly Pro Tyr Val Ser Val Pro Leu Asn Cys Ser Cys Gly Asp		
325	330	335
Thr Val Gln Ala Gln Leu His Asn Leu Glu Pro Cys Met Tyr Val Ala		
340	345	350
Val Val Ala His Gly Pro Ser Ile Leu Tyr Pro Ser Thr Val Trp Asp		
355	360	365
Phe Ile Asn Lys Lys Val Thr Val Gly Leu Tyr Gly Pro Lys His Ile		
370	375	380
His Pro Ser Phe Lys Thr Val Val Thr Ile Phe Gly His Asp Cys Ala		
385	390	395
Pro Lys Thr Leu Leu Val Ser Glu Val Thr Arg Gln Ala Pro Asn Pro		
405	410	415
Ala Pro Val Ala Leu Gln Leu Trp Gly Lys His Gln Phe Val Leu Ser		
420	425	430
Arg Pro Gln Asp Leu Lys Val Cys Met Phe Ser Asn Met Thr Asn Tyr		
435	440	445
Glu Val Lys Ala Ser Glu Gln Ala Lys Val Val Arg Gly Phe Gln Leu		
450	455	460
Lys Leu Gly Lys Val Ser Arg Leu Ile Phe Pro Ile Thr Ser Gln Asn		
465	470	475
Pro Asn Glu Leu Ser Asp Phe Thr Leu Arg Val Gln Val Lys Asp Asp		
485	490	495
Gln Glu Ala Ile Leu Thr Gln Phe Cys Val Gln Thr Pro Gln Pro Pro		

1241.22

500	505	510
Pro Lys Ser Ala Ile Lys Pro Ser Gly Gln Arg Arg Phe Leu Lys Lys		
515	520	525
Asn Glu Val Gly Lys Ile Ile Leu Ser Pro Phe Ala Thr Thr Thr Lys		
530	535	540
Tyr Pro Thr Phe Gln Asp Arg Pro Val Ser Ser Leu Lys Phe Gly Lys		
545	550	555
Leu Leu Lys Thr Val Val Arg Gln Asn Lys Asn His Tyr Leu Leu Glu		
565	570	575
Tyr Lys Lys Gly Asp Gly Ile Ala Leu Leu Ser Glu Glu Arg Val Arg		
580	585	590
Leu Arg Gly Gln Leu Trp Thr Lys Glu Trp Tyr Ile Gly Tyr Tyr Gln		
595	600	605
Gly Arg Val Gly Leu Val His Thr Lys Asn Val Leu Val Val Gly Arg		
610	615	620
Ala Arg Pro Ser Leu Cys Ser Gly Pro Glu Leu Ser Thr Ser Val Leu		
625	630	635
Leu Glu Gln Ile Leu Arg Pro Cys Lys Phe Leu Thr Tyr Ile Tyr Ala		
645	650	655
Ser Val Arg Thr Leu Leu Met Glu Asn Ile Ser Ser Trp Arg Ser Phe		
660	665	670
Ala Asp Ala Leu Gly Tyr Val Asn Leu Pro Leu Thr Phe Phe Cys Arg		
675	680	685
Ala Glu Leu Asp Ser Glu Pro Glu Arg Val Ala Ser Val Leu Glu Lys		
690	695	700
Leu Lys Glu Asp Cys Asn Asn Thr Glu Asn Lys Glu Arg Lys Ser Phe		
705	710	715
Gln Lys Glu Leu Val Met Ala Leu Leu Lys Met Asp Cys Gln Gly Leu		
725	730	735
Val Val Arg Leu Ile Gln Asp Phe Val Leu Leu Thr Thr Ala Val Glu		
740	745	750

1241.22

Val	Ala	Gln	Arg	Trp	Arg	Glu	Leu	Ala	Glu	Lys	Leu	Ala	Lys	Val	Ser
				755				760				765			
Lys	Gln	Gln	Met	Asp	Ala	Tyr	Glu	Ser	Pro	His	Arg	Asp	Arg	Asn	Gly
				770				775				780			
Val	Val	Asp	Ser	Glu	Ala	Met	Trp	Lys	Pro	Ala	Tyr	Asp	Phe	Leu	Leu
785				790				795				800			
Thr	Trp	Ser	His	Gln	Ile	Gly	Asp	Ser	Tyr	Arg	Asp	Val	Ile	Gln	Glu
				805				810				815			
Leu	His	Leu	Gly	Leu	Asp	Lys	Met	Lys	Asn	Pro	Ile	Thr	Lys	Arg	Trp
				820				825				830			
Lys	His	Leu	Thr	Gly	Thr	Leu	Ile	Leu	Val	Asn	Ser	Leu	Asp	Val	Leu
				835				840				845			
Arg	Ala	Ala	Ala	Phe	Ser	Pro	Ala	Asp	Gln	Asp	Asp	Phe	Val	Ile	
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<210> 153

<211> 2194

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (133)..(1125)

<400> 153

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tcgcttctcg ttctactgcc ccaggagccc ggcgggtccg ggactcccgt ccgtgccggt 120
gcgggcgccg gc atg tgg ctg tgg gag gac cag ggc ggc ctc ctg ggc cct 171
      Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro
          1             5             10
ttc tcc ttc ctg ctg cta gtg ctg ctg ctg gtg acg cgg agc ccg gtc   219
Phe Ser Phe Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val
      15             20             25
aat gcc tgc ctc ctc acc ggc agc ctc ttc gtt cta ctg cgc gtc ttc   267

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1241.22

Asn	Ala	Cys	Leu	Leu	Thr	Gly	Ser	Leu	Phe	Val	Leu	Leu	Arg	Val	Phe	
30					35				40						45	
agc	ttt	gag	ccg	gtg	ccc	tct	tgc	agg	gcc	ctg	cag	gtg	ctc	aag	ccc	315
Ser	Phe	Glu	Pro	Val	Pro	Ser	Cys	Arg	Ala	Leu	Gln	Val	Leu	Lys	Pro	
			50					55					60			
cgg	gac	cgc	att	tct	gcc	atc	gcc	cac	cgt	ggc	ggc	agc	cac	gac	gcg	363
Arg	Asp	Arg	Ile	Ser	Ala	Ile	Ala	His	Arg	Gly	Gly	Ser	His	Asp	Ala	
			65				70					75				
ccc	gag	aac	acg	ctg	gcg	gcc	att	cgg	cag	gca	gct	aag	aat	gga	gca	411
Pro	Glu	Asn	Thr	Leu	Ala	Ala	Ile	Arg	Gln	Ala	Ala	Lys	Asn	Gly	Ala	
		80					85					90				
aca	ggc	gtg	gag	ttg	gac	att	gag	ttt	act	tct	gac	ggg	att	cct	gtc	459
Thr	Gly	Val	Glu	Leu	Asp	Ile	Glu	Phe	Thr	Ser	Asp	Gly	Ile	Pro	Val	
	95					100						105				
tta	atg	cac	gat	aac	aca	gta	gat	agg	acg	act	gat	ggg	act	ggg	cga	507
Leu	Met	His	Asp	Asn	Thr	Val	Asp	Arg	Thr	Thr	Asp	Gly	Thr	Gly	Arg	
110					115					120				125		
ttg	tgt	gat	ttg	aca	ttt	gaa	caa	att	agg	aag	ctg	aat	cct	gca	gca	555
Leu	Cys	Asp	Leu	Thr	Phe	Glu	Gln	Ile	Arg	Lys	Leu	Asn	Pro	Ala	Ala	
			130						135				140			
aac	cac	aga	ctc	agg	aat	gat	ttc	cct	gat	gaa	aag	atc	cct	acc	cta	603
Asn	His	Arg	Leu	Arg	Asn	Asp	Phe	Pro	Asp	Glu	Lys	Ile	Pro	Thr	Leu	
			145					150				155				
agg	gaa	gct	gtt	gca	gag	tgc	cta	aac	cat	aac	ctc	aca	atc	ttc	ttt	651
Arg	Glu	Ala	Val	Ala	Glu	Cys	Leu	Asn	His	Asn	Leu	Thr	Ile	Phe	Phe	
		160					165					170				
gat	gtc	aaa	ggc	cat	gca	cac	aag	gct	act	gag	gct	cta	aag	aaa	atg	699
Asp	Val	Lys	Gly	His	Ala	His	Lys	Ala	Thr	Glu	Ala	Leu	Lys	Lys	Met	
		175				180					185					
tat	atg	gaa	ttt	cct	caa	ctg	tat	aat	aat	agt	gtg	gtc	tgt	tct	ttc	747
Tyr	Met	Glu	Phe	Pro	Gln	Leu	Tyr	Asn	Asn	Ser	Val	Val	Cys	Ser	Phe	
190					195					200					205	

1241.22

ttg cca gaa gtt atc tac aag atg aga caa aca gat cgg gat gta ata 795
Leu Pro Glu Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile
210 215 220
aca gca tta act cac aga cct tgg agc cta agc cat aca gga gat ggg 843
Thr Ala Leu Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly
225 230 235
aaa cca cgc tat gat act ttc tgg aaa cat ttt ata ttt gtt atg atg 891
Lys Pro Arg Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met
240 245 250
gac att ttg ctc gat tgg agc atg cat aat atc ttg tgg tac ctg tgt 939
Asp Ile Leu Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys
255 260 265
gga att tca gct ttc ctc atg caa aag gat ttt gta tcc ccg gcc tac 987
Gly Ile Ser Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr
270 275 280 285
ttg aag aag tgg tca gct aaa gga atc cag gtt gtt ggt tgg act gtt 1035
Leu Lys Lys Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val
290 295 300
aat acc ttt gat gaa aag agt tac tac gaa tcc cat ctt ggt tcc agc 1083
Asn Thr Phe Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser
305 310 315
tat atc act gac agc atg gta gaa gac tgc gaa cct cac ttc 1125
Tyr Ile Thr Asp Ser Met Val Glu Asp Cys Glu Pro His Phe
320 325 330
tagactttca cggtgggacg aaacgggttc agaaactgcc aggggcctca tacagggata 1185
tcaaaatacc ctttgtgcta gcccaggccc tggggaatca ggtgactcac acaaagcaaa 1245
tagttggtca ctgcattttt acctgaacca aagctaaacc cggtgttgcc accatgcacc 1305
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gagcccctgc cctgccctag ctgaggcaca caggagacc cagtgaggat aagcacagat 1425
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1241.22

tactgtagac atcaaacttg tggccatact aataaaatta ttaaaaggag cactaaagga 1605
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aaacttccaa aaatatctag gtttgcctc attttataaa tgaggaaact aaactctgtg 1905
gaaggggaagg ggttgccctca aaagtcacag cttagctggg cacagtggct catgccgata 1965
atcccagcaa ttcagaaagc tgaggcagga ggattacttg aggccagact gggcaatata 2025
gcaagacccc atctctaaaa aattagggcat ggtggtgcat gcctgtattc ccagctactc 2085
aggaggttga ggtgggagga tcacttgagc ccagaagttc aaggctgcaa tgagccatga 2145
ttacaccacg gcaactacaac cttggtggca cagtgagaac ctgactctt 2194

<210> 154

<211> 331

<212> PRT

<213> Homo sapiens

<400> 154

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20 25 30
Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu
35 40 45
Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg
50 55 60
Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala Pro Glu Asn
65 70 75 80
Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala Thr Gly Val
85 90 95
Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val Leu Met His
100 105 110
Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg Leu Cys Asp

1241.22

115	120	125
Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala Asn His Arg		
130	135	140
Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu Arg Glu Ala		
145	150	155
Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe Asp Val Lys		
165	170	175
Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met Tyr Met Glu		
180	185	190
Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe Leu Pro Glu		
195	200	205
Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile Thr Ala Leu		
210	215	220
Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly Lys Pro Arg		
225	230	235
Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met Asp Ile Leu		
245	250	255
Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys Gly Ile Ser		
260	265	270
Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr Leu Lys Lys		
275	280	285
Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val Asn Thr Phe		
290	295	300
Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser Tyr Ile Thr		
305	310	315
Asp Ser Met Val Glu Asp Cys Glu Pro His Phe		
325	330	

<210> 155

<211> 3377

<212> DNA

<213> Homo sapiens

1241.22

<220>

<221> CDS

<222> (44)..(1666)

<400> 155

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cag cga gtg gga gca gct gcc tca aga gga gca gat gat gcc atg gag 103
Gln Arg Val Gly Ala Ala Ala Ser Arg Gly Ala Asp Asp Ala Met Glu
  5             10             15             20
agc agc aag cct ggt cca gtg cag gtt gtt ttg gtt cag aaa gat caa 151
Ser Ser Lys Pro Gly Pro Val Gln Val Val Leu Val Gln Lys Asp Gln
             25             30             35
cat tcc ttt gag cta gat gag aaa gcc ttg gcc agc atc ctc ttg cag 199
His Ser Phe Glu Leu Asp Glu Lys Ala Leu Ala Ser Ile Leu Leu Gln
             40             45             50
gac cac atc cga gat ctt gat gtg gtg gtg gtt tca gtg gct ggt gcc 247
Asp His Ile Arg Asp Leu Asp Val Val Val Val Ser Val Ala Gly Ala
             55             60             65
ttc cga aag ggc aag tcc ttc att ctg gat ttt atg cta cga tac tta 295
Phe Arg Lys Gly Lys Ser Phe Ile Leu Asp Phe Met Leu Arg Tyr Leu
             70             75             80
tat tct cag aag gaa agt ggc cat tca aat tgg ttg ggt gac cca gaa 343
Tyr Ser Gln Lys Glu Ser Gly His Ser Asn Trp Leu Gly Asp Pro Glu
             85             90             95             100
gaa ccg tta aca gga ttt tcc tgg aga ggg gga tct gat cca gaa acc 391
Glu Pro Leu Thr Gly Phe Ser Trp Arg Gly Gly Ser Asp Pro Glu Thr
             105             110             115
act ggg att caa atc tgg agt gaa gtt ttc act gtg gag aag cca ggt 439
Thr Gly Ile Gln Ile Trp Ser Glu Val Phe Thr Val Glu Lys Pro Gly
             120             125             130
ggg aag aag gtt gca gtt gtt ctg atg gat acc cag ggg gca ttt gac 487
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1241.22

Gly Lys Lys Val Ala Val Val Leu Met Asp Thr Gln Gly Ala Phe Asp	
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Ser Gln Ser Thr Val Lys Asp Cys Ala Thr Ile Phe Ala Leu Ser Thr	
150 155 160	
atg act agt tct gtt cag att tat aat tta tct cag aac att caa gaa	583
Met Thr Ser Ser Val Gln Ile Tyr Asn Leu Ser Gln Asn Ile Gln Glu	
165 170 175 180	
gat gat ctt caa cag ctg cag ctc ttc aca gaa tac ggt cgt ctg gca	631
Asp Asp Leu Gln Gln Leu Gln Leu Phe Thr Glu Tyr Gly Arg Leu Ala	
185 190 195	
atg gat gaa att ttc caa aag cct ttc cag aca ctg atg ttt ttg gtt	679
Met Asp Glu Ile Phe Gln Lys Pro Phe Gln Thr Leu Met Phe Leu Val	
200 205 210	
aga gat tgg agt ttc cct tat gaa tat agc tat gga ctc caa gga gga	727
Arg Asp Trp Ser Phe Pro Tyr Glu Tyr Ser Tyr Gly Leu Gln Gly Gly	
215 220 225	
atg gca ttt ttg gat aag cgt tta cag gtg aag gaa cat caa cat gaa	775
Met Ala Phe Leu Asp Lys Arg Leu Gln Val Lys Glu His Gln His Glu	
230 235 240	
gaa att cag aat gtt cga aat cac att cac tca tgt ttc tcc gat gtc	823
Glu Ile Gln Asn Val Arg Asn His Ile His Ser Cys Phe Ser Asp Val	
245 250 255 260	
acc tgc ttt ctc tta cca cat cca gga ctc cag gtg gcc aca agc cct	871
Thr Cys Phe Leu Leu Pro His Pro Gly Leu Gln Val Ala Thr Ser Pro	
265 270 275	
gac ttt gat ggg aaa tta aaa gat att gct ggt gaa ttc aaa gag cag	919
Asp Phe Asp Gly Lys Leu Lys Asp Ile Ala Gly Glu Phe Lys Glu Gln	
280 285 290	
tta cag gca ctg ata ccg tat gta tta aac cca tct aag tta atg gaa	967
Leu Gln Ala Leu Ile Pro Tyr Val Leu Asn Pro Ser Lys Leu Met Glu	

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295	300	305		
aag gag atc aat ggc tca aag gtc acc tgt cgg gga cta ctg gag tat				1015
Lys Glu Ile Asn Gly Ser Lys Val Thr Cys Arg Gly Leu Leu Glu Tyr				
310	315	320		
ttt aag gca tat att aaa att tat caa gga gaa gat ctg cct cac ccc				1063
Phe Lys Ala Tyr Ile Lys Ile Tyr Gln Gly Glu Asp Leu Pro His Pro				
325	330	335	340	
aag tcc atg ctt cag gcc act gct gaa gcc aac aac tta gca gct gca				1111
Lys Ser Met Leu Gln Ala Thr Ala Glu Ala Asn Asn Leu Ala Ala Ala				
345	350	355		
gcc tct gcc aag gac att tat tat aac aac atg gaa gag gtt tgt ggg				1159
Ala Ser Ala Lys Asp Ile Tyr Tyr Asn Asn Met Glu Glu Val Cys Gly				
360	365	370		
gga gag aaa cct tat ttg tct cca gac att cta gag gag aag cac tgt				1207
Gly Glu Lys Pro Tyr Leu Ser Pro Asp Ile Leu Glu Glu Lys His Cys				
375	380	385		
gaa ttc aaa caa ctt gct ctg gac cat ttt aag aag acc aag aag atg				1255
Glu Phe Lys Gln Leu Ala Leu Asp His Phe Lys Lys Thr Lys Lys Met				
390	395	400		
ggg ggt aag gat ttc agc ttt cgt tac cag cag gag ctg gag gag gaa				1303
Gly Gly Lys Asp Phe Ser Phe Arg Tyr Gln Gln Glu Leu Glu Glu Glu				
405	410	415	420	
atc aag gaa tta tat gag aac ttc tgc aag cac aat ggt agc aag aac				1351
Ile Lys Glu Leu Tyr Glu Asn Phe Cys Lys His Asn Gly Ser Lys Asn				
425	430	435		
gtc ttc agc acc ttc cga acc cct gca gtg ctg ttc acg ggc att gta				1399
Val Phe Ser Thr Phe Arg Thr Pro Ala Val Leu Phe Thr Gly Ile Val				
440	445	450		
gct ttg tac ata gcc tca ggc ctc act ggc ttc ata ggt ctt gag gtt				1447
Ala Leu Tyr Ile Ala Ser Gly Leu Thr Gly Phe Ile Gly Leu Glu Val				
455	460	465		
gta gcc cag ttg ttc aac tgt atg gtt gga cta ctg tta ata gca ctc				1495

1241.22

Val Ala Gln Leu Phe Asn Cys Met Val Gly Leu Leu Ile Ala Leu
470 475 480
ctc acc tgg ggc tac atc agg tat tct ggt caa tat cgt gag ctg ggc 1543
Leu Thr Trp Gly Tyr Ile Arg Tyr Ser Gly Gln Tyr Arg Glu Leu Gly
485 490 495 500
gga gct att gat ttt ggt gcc gca tat gtg ttg gag cag gct tct tct 1591
Gly Ala Ile Asp Phe Gly Ala Ala Tyr Val Leu Glu Gln Ala Ser Ser
505 510 515
cat atc ggt aat tcc act cag gcc act gtg agg gat gca gtt gtt gga 1639
His Ile Gly Asn Ser Thr Gln Ala Thr Val Arg Asp Ala Val Val Gly
520 525 530
aga cca tcc atg gat aaa aaa gct caa tagcatctta acgtgaagat 1686
Arg Pro Ser Met Asp Lys Lys Ala Gln
535 540
caaacaagaa cacaacaagc ccctactgat ttctggggtt ctgccacggc cacaggttca 1746
tatccagagg aatggcagat ctgagacgat ccaggaagag ctaaaacatg gccctgtaat 1806
aaatgagcag acctctcctg tggtttcaaa ttattaaaca cacttccatt tctcttggaa 1866
gcatttcttt tccttgctgt tatagatgca agcctgtgtc tattttcata ttactctgct 1926
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ttgagtgcag tgggtgtgatc ttggctcact gcaacctctg cctgccgggt tcaagcagtt 2226
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cttgaccttg tgatccgcct gccgccttg gcctcccaaa gtgctgggat tacaggcgtg 2406
agccaccgtg cccggccaag aaggattcct tttttaaaag tttacagaac ttggagaaac 2466
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gaatcctgtt gccacatagt gtggaaaaat catgtcatat ttaaataac catactctga 2586
aatgtgaggt ttttaccag taggctgaca gttttgttgc aacttgctct attttttttt 2646
ttttttggtc cctatagctt ctttctagaa aaagaggcaa acgtgccttg aaaagccaga 2706

1241.22

gtggctcata ataaaaggaa tgcgctagat acttcaagaa aaaagctaag tttaaatagaa 2766
ccatgtgacc tctgataagt cacttgaact tgtgccttag tcaggttcac tgtaggttta 2826
catatgtatg tatgttttac acaactcttg taattgtcat ttgaggggtt cacttcctcc 2886
tcccaccccc tgggagcggc cctgcgctgt cactgacatc tcattaataaa aaaaaaaaaa 2946
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caagaattct ggctgtttac ctcagactca gacccttgaa atgttgccaa attcttcaaa 3066
taactgtttg gggggtgggg ggagatgaaa gagagtcgcg ttttgtttac agttaagac 3126
atccaatatc ttaaaaagga gttttccttt agaaacacac acacccttcc tcttgctcaa 3186
aagatctcac tccatgatac tgtgtaaaat atttttgcac tgttggaag tatttttgac 3246
ttttttctgt acataactgt gttctcagag ctgaatgttt atatcttttg ctgtgcaaaa 3306
gaaacatgta aaatgttggt cagttgtata tacagaaatg tgtataaaac attttggtat 3366
tttttaaaag t 3377

<210> 156

<211> 541

<212> PRT

<213> Homo sapiens

<400> 156

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			20					25					30		
Gln	Lys	Asp	Gln	His	Ser	Phe	Glu	Leu	Asp	Glu	Lys	Ala	Leu	Ala	Ser
		35					40					45			
Ile	Leu	Leu	Gln	Asp	His	Ile	Arg	Asp	Leu	Asp	Val	Val	Val	Val	Ser
	50				55				60						
Val	Ala	Gly	Ala	Phe	Arg	Lys	Gly	Lys	Ser	Phe	Ile	Leu	Asp	Phe	Met
	65				70				75					80	
Leu	Arg	Tyr	Leu	Tyr	Ser	Gln	Lys	Glu	Ser	Gly	His	Ser	Asn	Trp	Leu
			85					90					95		
Gly	Asp	Pro	Glu	Glu	Pro	Leu	Thr	Gly	Phe	Ser	Trp	Arg	Gly	Gly	Ser
		100						105					110		

1241.22

Asp Pro Glu Thr Thr Gly Ile Gln Ile Trp Ser Glu Val Phe Thr Val
115 120 125

Glu Lys Pro Gly Gly Lys Lys Val Ala Val Val Leu Met Asp Thr Gln
130 135 140

Gly Ala Phe Asp Ser Gln Ser Thr Val Lys Asp Cys Ala Thr Ile Phe
145 150 155 160

Ala Leu Ser Thr Met Thr Ser Ser Val Gln Ile Tyr Asn Leu Ser Gln
165 170 175

Asn Ile Gln Glu Asp Asp Leu Gln Gln Leu Gln Leu Phe Thr Glu Tyr
180 185 190

Gly Arg Leu Ala Met Asp Glu Ile Phe Gln Lys Pro Phe Gln Thr Leu
195 200 205

Met Phe Leu Val Arg Asp Trp Ser Phe Pro Tyr Glu Tyr Ser Tyr Gly
210 215 220

Leu Gln Gly Gly Met Ala Phe Leu Asp Lys Arg Leu Gln Val Lys Glu
225 230 235 240

His Gln His Glu Glu Ile Gln Asn Val Arg Asn His Ile His Ser Cys
245 250 255

Phe Ser Asp Val Thr Cys Phe Leu Leu Pro His Pro Gly Leu Gln Val
260 265 270

Ala Thr Ser Pro Asp Phe Asp Gly Lys Leu Lys Asp Ile Ala Gly Glu
275 280 285

Phe Lys Glu Gln Leu Gln Ala Leu Ile Pro Tyr Val Leu Asn Pro Ser
290 295 300

Lys Leu Met Glu Lys Glu Ile Asn Gly Ser Lys Val Thr Cys Arg Gly
305 310 315 320

Leu Leu Glu Tyr Phe Lys Ala Tyr Ile Lys Ile Tyr Gln Gly Glu Asp
325 330 335

Leu Pro His Pro Lys Ser Met Leu Gln Ala Thr Ala Glu Ala Asn Asn
340 345 350

Leu Ala Ala Ala Ala Ser Ala Lys Asp Ile Tyr Tyr Asn Asn Met Glu
355 360 365

1241.22

Glu Val Cys Gly Gly Glu Lys Pro Tyr Leu Ser Pro Asp Ile Leu Glu
370 375 380
Glu Lys His Cys Glu Phe Lys Gln Leu Ala Leu Asp His Phe Lys Lys
385 390 395 400
Thr Lys Lys Met Gly Gly Lys Asp Phe Ser Phe Arg Tyr Gln Gln Glu
405 410 415
Leu Glu Glu Glu Ile Lys Glu Leu Tyr Glu Asn Phe Cys Lys His Asn
420 425 430
Gly Ser Lys Asn Val Phe Ser Thr Phe Arg Thr Pro Ala Val Leu Phe
435 440 445
Thr Gly Ile Val Ala Leu Tyr Ile Ala Ser Gly Leu Thr Gly Phe Ile
450 455 460
Gly Leu Glu Val Val Ala Gln Leu Phe Asn Cys Met Val Gly Leu Leu
465 470 475 480
Leu Ile Ala Leu Leu Thr Trp Gly Tyr Ile Arg Tyr Ser Gly Gln Tyr
485 490 495
Arg Glu Leu Gly Gly Ala Ile Asp Phe Gly Ala Ala Tyr Val Leu Glu
500 505 510
Gln Ala Ser Ser His Ile Gly Asn Ser Thr Gln Ala Thr Val Arg Asp
515 520 525
Ala Val Val Gly Arg Pro Ser Met Asp Lys Lys Ala Gln
530 535 540

<210> 157

<211> 2172

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (45)..(563)

<400> 157

ggaacacggc acccgactg cgcgtcatgg tgcaggcctg gtat atg gac gac gcc 56

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Met Asp Asp Ala

1

ccg ggc gac ccg cgg caa ccc cac cgc ccc gac ccc ggc cgc cca gtg	104
Pro Gly Asp Pro Arg Gln Pro His Arg Pro Asp Pro Gly Arg Pro Val	
5 10 15 20	
ggc ctg gag cag ctg cgg cgg ctc ggg gtg ctc tac tgg aag ctg gat	152
Gly Leu Glu Gln Leu Arg Arg Leu Gly Val Leu Tyr Trp Lys Leu Asp	
25 30 35	
gct gac aaa tat gag aat gat cca gaa tta gaa aag atc cga aga gag	200
Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Arg Glu	
40 45 50	
agg aac tac tcc tgg atg gac atc ata acc ata tgc aaa gat aaa cta	248
Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Lys Leu	
55 60 65	
cca aat tat gaa gaa aag att aag atg ttc tac gag gag cat ttg cac	296
Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu Glu His Leu His	
70 75 80	
ttg gac gat gag atc cgc tac atc ctg gat ggc agt ggg tac ttc gat	344
Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser Gly Tyr Phe Asp	
85 90 95 100	
gtg agg gac aag gag gac cag tgg atc cgg atc ttc atg gag aag gga	392
Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe Met Glu Lys Gly	
105 110 115	
gac atg gtg acg ctc ccc gcg ggg atc tat cac cgc ttc acg gtg gac	440
Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Val Asp	
120 125 130	
gag aag aac tac acg aag gcc atg cgg ctg ttt gtg gga gaa ccg gtg	488
Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val	
135 140 145	
tgg aca gcg tac aac cgg ccc gct gac cat ttt gaa gcc cgc ggg cag	536
Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu Ala Arg Gly Gln	

		1241.22	
150	155	160	
tac gtg aaa ttt ctg gca cag acc gcc tagcagtgct gcctgggaac			583
Tyr Val Lys Phe Leu Ala Gln Thr Ala			
165	170		
taacacgtgc ctcgtaaagg tccccaatgt aatgactgag cagaaaatca atcactttct	643		
ctttgctttt agaggatagc cttgaggcta gattatcttt ctttgtaag attatttgat	703		
cagaatattt tgtaatgaaa ggatctagaa agcaacttg aagtgtaaag agtcaccttc	763		
atcttctgta actcaatcaa gactggtggg tccatggccc tgtgttagtt catgcattca	823		
gttgagtccc aaatgaaagt ttcattctccc gaaatgcagt tccttagatg cccatctgga	883		
cgtgatgccg cgcttgccgt gtaagaagg gcaatcctag ataacacagc tagccagata	943		
gaagacactt ttttctccaa aatgatgcct tgggggtgggg agtggtaggg ggaagagctc	1003		
ccaccctaag gggcacacac tgagttgctt atgccacttc cttgttcaaa ataaagtaac	1063		
tgccttaatc ttatactcat ggcttgaggt taccttatat tcaggatatat gtgatatttt	1123		
gcctggtttg ttaaaattgc cccatttaga ttccttctat aattgttctt atagataagt	1183		
aatttatata tgagctgtgt tagtattttt tcagtgtgag atctctggat tctttcacia	1243		
taaagctgtt gaattttaac aggagtatta gtacataaat tttctactca acaattccga	1303		
gataggatta tgcctagttt gtcatatcac agaaaaactc caagttaact tcatgttttg	1363		
gaagggcagg tcgtttttta agtatttctt tttttaactg gatgaaaaat cttcatgtta	1423		
ggattaattt tcttaatcac ctccacactg tacagaggaa actcaagcct taaatgttta	1483		
agtaaactct gtctcagttt taggattaaa ataccaccg gtggtgtgat gatgccatat	1543		
accgcagggc ttgcttctgt caagtgtgac tctatctcag taattaaaat aagtgtgat	1603		
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ttttaagaac gaaacattca tatgataaac tatcgcttta aattgccttt cttgcttcat	1723		
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tttttacagg caagagtaag ttcctgggca cagtggctca tgcctgtaat ctgagctact	1903		
caggaggcta aggtgggagg attcttagag cctgggaggt cgaggctgca gtgagctgtg	1963		
attgtggcca ctgcactcca gcctgggtga cagagcgaga ctctgtctca aaaaagaaga	2023		
aagagtaaga gctgaggcat ataatagaat tctgctaaag cacttaaggt gaaatcacat	2083		
tttcttttcc caggatgttg ctacatctt tcgtttttat tgagggtgtca tttatgtaca	2143		
ataaaatgta ctcatcttca gtgtttttg	2172		

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<210> 158

<211> 173

<212> PRT

<213> Homo sapiens

<400> 158

Met Asp Asp Ala Pro Gly Asp Pro Arg Gln Pro His Arg Pro Asp Pro
1 5 10 15
Gly Arg Pro Val Gly Leu Glu Gln Leu Arg Arg Leu Gly Val Leu Tyr
20 25 30
Trp Lys Leu Asp Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys
35 40 45
Ile Arg Arg Glu Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys
50 55 60
Lys Asp Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu
65 70 75 80
Glu His Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser
85 90 95
Gly Tyr Phe Asp Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe
100 105 110
Met Glu Lys Gly Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg
115 120 125
Phe Thr Val Asp Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val
130 135 140
Gly Glu Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu
145 150 155 160
Ala Arg Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala
165 170

<210> 159

<211> 20

<212> DNA

<220>



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<223> Description of the artificial sequence:an artificially synthesized primer sequence

<400> 159

ggaagtgtta cttctgctct

20

<210> 160

<211> 50

<212> DNA

<220>

<223> Description of the artificial sequence:an artificially synthesized primer sequence

<400> 160

gagagagaga gagagagaga actagtctcg agtttttttt tttttttttt

50

<210> 161

<211> 41

<212> DNA

<220>

<223> Description of the artificial sequence:an artificially synthesized primer sequence

<400> 161

gagagagaga gagagagcgg ccgcactagt ccccccccc c

41

<210> 162

<211> 30

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence: an artificially synthesized oligo-cap linker sequence

<400> 162

agcaucgagu cgccuuguu ggccuacugg

30

<210> 163

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence: an artificially synthesized oligo(dT)primer sequence

<400> 163

gcggctgaag acggcctatg tggccttttt tttttttttt tt

42


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<210> 164
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of the artificial sequence: an artificially synthesized primer
sequence
<400> 164
agcatcgagt cggccttggt g                                21

<210> 165
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of the artificial sequence: an artificially synthesized primer
sequence
<400> 165
gcggctgaag acggcctatg t                                21

<210> 166
<211> 30
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of the artificial sequence: an artificially synthesized primer
sequence
<400> 166
actttattgt catagtttag atctattttg                        30

<210> 167
<211> 30
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of the artificial sequence: an artificially synthesized primer
sequence
<400> 167
ataatcctta aaaactccat ttccaccctt                        30

<210> 168
<211> 1536
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (139)..(1062)
<400> 168
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agcgaagagc ggcctcctga gggaggggaa gggacgtggg ggcggccacg gcaggattaa        120
cctccatttc agctaate atg gga gag att aaa gtc tct cct gat tat aac          171
               Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn
                   1               5               10

tgg ttt aga ggt aca gtt ccc ctt aaa aag att att gtg gat gat gat          219
Trp Phe Arg Gly Thr Val Pro Leu Lys Lys Ile Ile Val Asp Asp Asp
                   15               20               25

gac agt aag ata tgg tcg ctc tat gac gcg ggc ccc cga agt atc agg          267
Asp Ser Lys Ile Trp Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg
                   30               35               40

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1241.22

tgt	cct	ctc	ata	ttc	ctg	ccc	cct	gtc	agt	gga	act	gca	gat	gtc	ttt	315
Cys	Pro	Leu	Ile	Phe	Leu	Pro	Pro	Val	Ser	Gly	Thr	Ala	Asp	Val	Phe	
	45					50					55					
ttc	cgg	cag	att	ttg	gct	ctg	act	gga	tgg	ggt	tac	cgg	ggt	atc	gct	363
Phe	Arg	Gln	Ile	Leu	Ala	Leu	Thr	Gly	Trp	Gly	Tyr	Arg	Val	Ile	Ala	
60					65					70					75	
ttg	cag	tat	cca	gtt	tat	tgg	gac	cat	ctc	gag	ttc	tgt	gat	gga	ttc	411
Leu	Gln	Tyr	Pro	Val	Tyr	Trp	Asp	His	Leu	Glu	Phe	Cys	Asp	Gly	Phe	
				80					85					90		
aga	aaa	ctt	tta	gac	cat	tta	caa	ttg	gat	aaa	ggt	cat	ctt	ttt	ggc	459
Arg	Lys	Leu	Leu	Asp	His	Leu	Gln	Leu	Asp	Lys	Val	His	Leu	Phe	Gly	
			95					100					105			
gct	tct	ttg	gga	ggc	ttt	ttg	gcc	cag	aaa	ttt	gct	gaa	tat	act	cac	507
Ala	Ser	Leu	Gly	Gly	Phe	Leu	Ala	Gln	Lys	Phe	Ala	Glu	Tyr	Thr	His	
		110					115					120				
aaa	tct	cct	aga	gtc	cat	tcc	cta	atc	ctc	tgc	aat	tcc	ttc	agt	gac	555
Lys	Ser	Pro	Arg	Val	His	Ser	Leu	Ile	Leu	Cys	Asn	Ser	Phe	Ser	Asp	
	125					130					135					
acc	tct	atc	ttc	aac	caa	act	tgg	act	gca	aac	agc	ttt	tgg	ctg	atg	603
Thr	Ser	Ile	Phe	Asn	Gln	Thr	Trp	Thr	Ala	Asn	Ser	Phe	Trp	Leu	Met	
140					145					150					155	
cct	gca	ttt	atg	ctc	aaa	aaa	ata	gtt	ctt	gga	aat	ttt	tca	tct	ggc	651
Pro	Ala	Phe	Met	Leu	Lys	Lys	Ile	Val	Leu	Gly	Asn	Phe	Ser	Ser	Gly	
				160					165					170		
ccg	gtg	gac	cct	atg	atg	gct	gat	gcc	att	gat	ttc	atg	gta	gac	agg	699
Pro	Val	Asp	Pro	Met	Met	Ala	Asp	Ala	Ile	Asp	Phe	Met	Val	Asp	Arg	
			175					180					185			
cta	gaa	agt	ttg	ggt	cag	agt	gaa	ctg	gct	tca	aga	ctt	acc	ttg	aat	747
Leu	Glu	Ser	Leu	Gly	Gln	Ser	Glu	Leu	Ala	Ser	Arg	Leu	Thr	Leu	Asn	
		190					195					200				
tgt	caa	aat	tct	tat	gtg	gta	cct	cat	aaa	att	cgg	gac	ata	cct	gta	795
Cys	Gln	Asn	Ser	Tyr	Val	Val	Pro	His	Lys	Ile	Arg	Asp	Ile	Pro	Val	
	205					210					215					
act	att	atg	gat	gtg	ttt	gat	cag	agt	gcg	ctt	tca	act	gaa	gct	aaa	843
Thr	Ile	Met	Asp	Val	Phe	Asp	Gln	Ser	Ala	Leu	Ser	Thr	Glu	Ala	Lys	
220					225					230					235	
gaa	gaa	atg	tac	aag	ctg	tat	cct	aat	gcc	cga	aga	gct	cat	ctg	aaa	891
Glu	Glu	Met	Tyr	Lys	Leu	Tyr	Pro	Asn	Ala	Arg	Arg	Ala	His	Leu	Lys	
				240					245					250		
aca	gga	ggc	aat	ttc	cca	tac	ctg	tgc	aga	agt	gca	gag	gtc	aat	ctt	939
Thr	Gly	Gly	Asn	Phe	Pro	Tyr	Leu	Cys	Arg	Ser	Ala	Glu	Val	Asn	Leu	
			255					260					265			
tat	gta	cag	ata	cat	ttg	ctg	caa	ttc	cat	gga	acc	aaa	tac	gcg	gcc	987
Tyr	Val	Gln	Ile	His	Leu	Leu	Gln	Phe	His	Gly	Thr	Lys	Tyr	Ala	Ala	
		270					275					280				
att	gac	cca	tca	atg	gtc	agt	gcc	gag	gag	ctt	gag	gtg	cag	aaa	ggc	1035
Ile	Asp	Pro	Ser	Met	Val	Ser	Ala	Glu	Glu	Leu	Glu	Val	Gln	Lys	Gly	
	285					290					295					

1241.22

agc ctt ggc atc agc cag gag gag cag tagtgtgtct ctcgctgtca atgatga 1089
 Ser Leu Gly Ile Ser Gln Glu Glu Gln
 300 305

gttgaccgg tgtgttcttg tatagtcagt ggcattcagca cccgtcagcc ggccttttcc 1149
 ttcaggttcg tcaggctcac cggttctcac tgtgtctggg aagtaggact gatgggtcac 1209
 ttcattgacag gcggcatctc cactaagcct gtgtaactgt tccctctttg gttttcttag 1269
 cttttgaatt tgaagaagta cttttgaaga ctccattttt aagaaccgtg cagattttgc 1329
 taccaaaagt cttcaccact gtgttcttaa gtgaatgtta atttctgagg tttgggactt 1389
 tgtggtggtt tttttcttct tttcttttcc atttctcttt ctttcttttt atgttggtttg 1449
 ctgtaaagtc tgacatcca gattgcatat caggacattg gttattttat gctttcttgg 1509
 atataacat gatcagagtg ccatggc 1536

<210> 169

<211> 308

<212> PRT

<213> Homo sapiens

<400> 169

Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn Trp Phe Arg Gly Thr
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 20 25 30
 Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe
 35 40 45
 Leu Pro Pro Val Ser Gly Thr Ala Asp Val Phe Phe Arg Gln Ile Leu
 50 55 60
 Ala Leu Thr Gly Trp Gly Tyr Arg Val Ile Ala Leu Gln Tyr Pro Val
 65 70 75 80
 Tyr Trp Asp His Leu Glu Phe Cys Asp Gly Phe Arg Lys Leu Leu Asp
 85 90 95
 His Leu Gln Leu Asp Lys Val His Leu Phe Gly Ala Ser Leu Gly Gly
 100 105 110
 Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His Lys Ser Pro Arg Val
 115 120 125
 His Ser Leu Ile Leu Cys Asn Ser Phe Ser Asp Thr Ser Ile Phe Asn
 130 135 140
 Gln Thr Trp Thr Ala Asn Ser Phe Trp Leu Met Pro Ala Phe Met Leu
 145 150 155 160
 Lys Lys Ile Val Leu Gly Asn Phe Ser Ser Gly Pro Val Asp Pro Met
 165 170 175
 Met Ala Asp Ala Ile Asp Phe Met Val Asp Arg Leu Glu Ser Leu Gly
 180 185 190
 Gln Ser Glu Leu Ala Ser Arg Leu Thr Leu Asn Cys Gln Asn Ser Tyr
 195 200 205
 Val Val Pro His Lys Ile Arg Asp Ile Pro Val Thr Ile Met Asp Val
 210 215 220
 Phe Asp Gln Ser Ala Leu Ser Thr Glu Ala Lys Glu Glu Met Tyr Lys
 225 230 235 240
 Leu Tyr Pro Asn Ala Arg Arg Ala His Leu Lys Thr Gly Gly Asn Phe
 245 250 255
 Pro Tyr Leu Cys Arg Ser Ala Glu Val Asn Leu Tyr Val Gln Ile His
 260 265 270
 Leu Leu Gln Phe His Gly Thr Lys Tyr Ala Ala Ile Asp Pro Ser Met
 275 280 285
 Val Ser Ala Glu Glu Leu Glu Val Gln Lys Gly Ser Leu Gly Ile Ser
 290 295 300
 Gln Glu Glu Gln
 305

<210> 170

1241.22

<211> 2560

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (202)..(1002)

<400> 170

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tgcagttgaa	gcagaaccaa	gtggccatcc	cggcgttaga	ccgtaggttc	ctgggtcccgg	120
agtggtcgga	gcccgccagt	gggcaggcag	ctcttgctca	caggccgcgg	tgcccaggcc	180
gctggctctc	cgcagggcgg	a atg gcg	ctg caa gtg	gag ctg gta	ccc acc	231
		Met Ala	Leu Gln Val	Glu Leu Val	Pro Thr	
		1		5	10	

ggg gag atc atc cgc	gtg gtt cat ccc	cac agg ccc	tgc aag ctt gcc	279
Gly Glu Ile Ile Arg	Val Val His Pro	His Arg Pro Cys	Lys Leu Ala	
	15	20	25	

ctg ggc agt gac ggg	gtt cgg gtg acc	atg gag agt gcg	ctc acc gcc	327
Leu Gly Ser Asp Gly	Val Arg Val Thr	Met Glu Ser Ala	Leu Thr Ala	
	30	35	40	

cgt gac cgg gtg ggg	gtg cag gat ttc	gtg ctg ctg gag	aac ttc acc	375
Arg Asp Arg Val Gly	Val Gln Asp Phe	Val Leu Leu Glu	Asn Phe Thr	
	45	50	55	

agc gag gcc gcc ttc	atc ggg aac ctg	cgg cgg cga ttt	cgg gag aat	423
Ser Glu Ala Ala Phe	Ile Gly Asn Leu	Arg Arg Arg Phe	Arg Glu Asn	
	60	65	70	

ctc atc tac acc tac	att ggc ccc gtc	ctg gtc tct gtc	aat ccc tac	471
Leu Ile Tyr Thr Tyr	Ile Gly Pro Val	Leu Val Ser Val	Asn Pro Tyr	
	80	85	90	

cgg gac ctg cag atc	tac agc cgg cag	cat atg gag cgt	tac cgt ggc	519
Arg Asp Leu Gln Ile	Tyr Ser Arg Gln	His Met Glu Arg	Tyr Arg Gly	
	95	100	105	

gtc agc ttc tat gaa	gtg ccc cct cac	ctg ttt gcc gtg	gcg gac act	567
Val Ser Phe Tyr Glu	Val Pro Pro His	Leu Phe Ala Val	Ala Asp Thr	
	110	115	120	

gtg tac cga gca ctg	cgc acg gag cgt	cgg gac cag gct	gtg atg atc	615
Val Tyr Arg Ala Leu	Arg Thr Glu Arg	Asp Gln Ala Val	Met Ile	
	125	130	135	

tct ggg gag agc ggg	gca ggc aag acc	gag gcc acc aag	agg ctg ctg	663
Ser Gly Glu Ser Gly	Ala Gly Lys Thr	Glu Ala Thr Lys	Arg Leu Leu	
	140	145	150	

cag ttc tat gca gag	acc tgc cca gcc	ccc gag cgc gga	ggt gcc gtg	711
Gln Phe Tyr Ala Glu	Thr Cys Pro Ala	Pro Glu Arg Gly	Gly Ala Val	
	155	160	165	170

cgg gac cgg ctg cta	cag agc aac ccg	gtg ctg gag gcc	ttt gga aat	759
Arg Asp Arg Leu Leu	Gln Ser Asn Pro	Val Leu Glu Ala	Phe Gly Asn	
	175	180	185	

gcc aag acc ctc cgg	aac gat aac tcc	agc agg ttc ggg	aag tac atg	807
Ala Lys Thr Leu Arg	Asn Asp Asn Ser	Arg Phe Gly Lys	Tyr Met	
	190	195	200	

gat gtg cag ttt gac	ttc aag ggt gcc	ccc gtg ggt ggc	cac atc ctc	855
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1241.22

Asp	Val	Gln	Phe	Asp	Phe	Lys	Gly	Ala	Pro	Val	Gly	Gly	His	Ile	Leu	
		205					210					215				
agt	tac	ccc	ctg	gaa	aag	tca	cga	gtg	gtg	cac	cag	aat	cat	ggg	gag	903
Ser	Tyr	Pro	Leu	Glu	Lys	Ser	Arg	Val	Val	His	Gln	Asn	His	Gly	Glu	
	220					225					230					
cgg	aac	ttc	aca	tct	tct	acc	agc	tgc	tgg	agg	ggg	gcg	agg	agg	aga	951
Arg	Asn	Phe	Thr	Ser	Ser	Thr	Ser	Cys	Trp	Arg	Gly	Ala	Arg	Arg	Arg	
235					240					245					250	
ctc	ttc	gca	ggc	tgg	gct	tgg	aac	gga	acc	ccc	aga	gct	atc	tgt	acc	999
Leu	Phe	Ala	Gly	Trp	Ala	Trp	Asn	Gly	Thr	Pro	Arg	Ala	Ile	Cys	Thr	
				255				260						265		
tgg	tgaaggccag	tgtgccaag	tcttcttcat	caacgacaag	agtgactgga	aggtcg										1058
Trp																
tcaggaaggc	tctgacagtc	attgatttca	ccgaggatga	agtggaggac	ctgctgagca											1118
tcgtggccag	cgtccttcat	ttgggcaaca	tccactttgc	tgccaacgag	gagagcaatg											1178
cccaggtcac	caccgagaac	cagctcaagt	atctgagccc	attcagtatg	cgggtgcctgt											1238
tgtgaaatac	gaccgcaagg	gctacaagcc	tcgctcccg	cagctgctgc	tcacgccccaa											1298
cgccgtcgtc	atcgtggagg	acgccaaagt	caagcagagg	attgattacg	ccaacctgac											1358
cggaatctct	gtcagcagcc	tgagcgacag	tctttttgtg	cttcatgtac	agcgtgcgga											1418
caataagcaa	aagggagatg	tgggtgctga	gagtgaccac	gtgattgaga	cgctgaccaa											1478
gacagccctc	agtgcccaacc	gcgtgaacag	catcaacatc	aaccagggca	gcatcacggt											1538
tgcagggggc	cccggcagg	atggcaccat	tgacttcaca	cccggctcgg	agctgctcat											1598
caccaaggcc	aagaacgggc	acctggctgt	ggtcgcccc	cggctgaatt	ctcggtgata											1658
aaggcgcccc	ctggaccctc	ccaacgcccc	atgctttgct	tttctcctcc	tccccttccc											1718
agttaccaaa	gactcgaact	tccagacagg	gaccagggga	caccccgagg	cccacctgca											1778
atctcccacc	tcttgcccat	ccctctcttg	aggagcagc	aggggccagg	agctaccccc											1838
ggagtggggc	aggccggg	acagcaatag	gaaagccagg	gccagagcga	gccatgccag											1898
ccctactgcc	gatgccaaat	atttgagaga	agggaacttt	tgctgaggtt	ttctctgagg											1958
ttttttttga	tgcttttatag	gaaactat	tttaaaaaaa	gccatttccc	acccaaggac											2018
acagtggatg	tggtttccct	gactccagca	gggcaaggaa	atgtagccga	gaggttgtgt											2078
gggctgggct	ctgggtgccct	cttccctggc	caggacacct	ctcctcctga	ttcccttggc											2138
acctgtgtct	tctgtctgtt	tacctgtctc	cctgcctgcc	catctgcctc	ttttgcagcc											2198
cactctgact	tccatctggg	ggctgagacc	accttgcct	gcccccttct	ttctgcctta											2258
agaatgtcct	tttaggctgg	gcatgggtgg	tcacgcctgt	aaccccgagca	ctttgggagg											2318
cggagacggg	cagataacct	gaggtcagga	tttcgagacc	aacctgacct	acatggagaa											2378
actccgctc	tggttaaggat	acaaaattag	ccgggcatgg	tggtgcacgc	ctctaattccc											2438
agctgctcgg	gaggctgagg	caggagaatc	acttgaaccc	gggaagtgg	gggtgcagtg											2498
agccaagagt	acaccactgc	actccagcct	gggcaacaga	gcgagactcc	gtcttaaaaa											2558
aa																2560

<210> 171
 <211> 267
 <212> PRT
 <213> Homo sapiens
 <400> 171

Met	Ala	Leu	Gln	Val	Glu	Leu	Val	Pro	Thr	Gly	Glu	Ile	Ile	Arg	Val	
1					5				10					15		
Val	His	Pro	His	Arg	Pro	Cys	Lys	Leu	Ala	Leu	Gly	Ser	Asp	Gly	Val	
			20				25						30			
Arg	Val	Thr	Met	Glu	Ser	Ala	Leu	Thr	Ala	Arg	Asp	Arg	Val	Gly	Val	
		35					40					45				
Gln	Asp	Phe	Val	Leu	Leu	Glu	Asn	Phe	Thr	Ser	Glu	Ala	Ala	Phe	Ile	
	50					55					60					
Gly	Asn	Leu	Arg	Arg	Arg	Phe	Arg	Glu	Asn	Leu	Ile	Tyr	Thr	Tyr	Ile	
	65				70				75						80	
Gly	Pro	Val	Leu	Val	Ser	Val	Asn	Pro	Tyr	Arg	Asp	Leu	Gln	Ile	Tyr	
				85					90					95		

1241.22

Ser	Arg	Gln	His	Met	Glu	Arg	Tyr	Arg	Gly	Val	Ser	Phe	Tyr	Glu	Val
			100					105					110		
Pro	Pro	His	Leu	Phe	Ala	Val	Ala	Asp	Thr	Val	Tyr	Arg	Ala	Leu	Arg
		115					120					125			
Thr	Glu	Arg	Arg	Asp	Gln	Ala	Val	Met	Ile	Ser	Gly	Glu	Ser	Gly	Ala
	130				135						140				
Gly	Lys	Thr	Glu	Ala	Thr	Lys	Arg	Leu	Leu	Gln	Phe	Tyr	Ala	Glu	Thr
145					150					155					160
Cys	Pro	Ala	Pro	Glu	Arg	Gly	Gly	Ala	Val	Arg	Asp	Arg	Leu	Leu	Gln
			165						170					175	
Ser	Asn	Pro	Val	Leu	Glu	Ala	Phe	Gly	Asn	Ala	Lys	Thr	Leu	Arg	Asn
		180						185					190		
Asp	Asn	Ser	Ser	Arg	Phe	Gly	Lys	Tyr	Met	Asp	Val	Gln	Phe	Asp	Phe
		195					200					205			
Lys	Gly	Ala	Pro	Val	Gly	Gly	His	Ile	Leu	Ser	Tyr	Pro	Leu	Glu	Lys
	210					215					220				
Ser	Arg	Val	Val	His	Gln	Asn	His	Gly	Glu	Arg	Asn	Phe	Thr	Ser	Ser
225					230					235					240
Thr	Ser	Cys	Trp	Arg	Gly	Ala	Arg	Arg	Arg	Leu	Phe	Ala	Gly	Trp	Ala
			245					250						255	
Trp	Asn	Gly	Thr	Pro	Arg	Ala	Ile	Cys	Thr	Trp					
		260						265							

<210> 172
 <211> 2560
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222>(116)..(1216)
 <400> 172

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cgcggtccag	gcgggagggcg	actccctagg	aagggacccg	gggcgggagg	aggaa atg	118
					Met	
					1	
agg ccg cgc gga agg aag gcg gcg agc ccc ggg gcc ccg agg cct tgg	166					
Arg Pro Arg Gly Arg Lys Ala Ala Ser Pro Gly Ala Pro Arg Pro Trp						
	5 10 15					
ccg cgt cac agc acc cac atg gcc tct gga gtg ggc gcg gcc ttc gag	214					
Pro Arg His Ser Thr His Met Ala Ser Gly Val Gly Ala Ala Phe Glu						
	20 25 30					
gaa ctg cct cac gac ggc acg tgt gac gag tgc gag ccc gac gag gct	262					
Glu Leu Pro His Asp Gly Thr Cys Asp Glu Cys Glu Pro Asp Glu Ala						
	35 40 45					
ccg ggg gcc gag gaa gtg tgc cga gaa tgc ggc ttc tgc tac tgc cgc	310					
Pro Gly Ala Glu Glu Val Cys Arg Glu Cys Gly Phe Cys Tyr Cys Arg						
	50 55 60 65					
cgc cat gcc gag gcg cac agg cag aag ttc ctc agt cac cat ctg gcc	358					
Arg His Ala Glu Ala His Arg Gln Lys Phe Leu Ser His His Leu Ala						
	70 75 80					
gaa tac gtc cac ggc tcc cag gcc tgg acc ccg cca gct gac gga gag	406					
Glu Tyr Val His Gly Ser Gln Ala Trp Thr Pro Pro Ala Asp Gly Glu						
	85 90 95					
ggg gcg ggg aag gaa gaa gcg gag gtc aag gtg gag cag gag agg gag	454					
Gly Ala Gly Lys Glu Glu Ala Glu Val Lys Val Glu Gln Glu Arg Glu						
	100 105 110					

1241.22

ata gaa agc gag gca ggg gaa gag agt gag tgc gag gaa gag agc gag Ile Glu Ser Glu Ala Gly Glu Glu Ser Glu Ser Glu Glu Glu Ser Glu 115 120 125	502
tca gag gaa gag agc gag aca gag gaa gag agt gag gat gag agc gat Ser Glu Glu Glu Ser Glu Thr Glu Glu Glu Ser Glu Asp Glu Ser Asp 130 135 140 145	550
gag gag agt gaa gaa gac agc gag gaa gaa atg gag gat gag caa gaa Glu Glu Ser Glu Glu Asp Ser Glu Glu Glu Met Glu Asp Glu Gln Glu 150 155 160	598
agc gag gcc gaa gaa gac aac caa gaa gaa ggg gaa tcc gag gcg gag Ser Glu Ala Glu Glu Asp Asn Gln Glu Glu Gly Glu Ser Glu Ala Glu 165 170 175	646
gga gaa act gag gca gaa agt gaa ttt gac cca gaa ata gaa atg gaa Gly Glu Thr Glu Ala Glu Ser Glu Phe Asp Pro Glu Ile Glu Met Glu 180 185 190	694
gca gag aga gtg gcc aag agg aag tgt ccg gac cat ggg ctt gat ttg Ala Glu Arg Val Ala Lys Arg Lys Cys Pro Asp His Gly Leu Asp Leu 195 200 205	742
agt acc tat tgc cag gaa gat agg cag ctc atc tgt gtc ctg tgt cca Ser Thr Tyr Cys Gln Glu Asp Arg Gln Leu Ile Cys Val Leu Cys Pro 210 215 220 225	790
gtc att ggg gct cac cag ggc cac caa ctc tcc acc cta gac gaa gcc Val Ile Gly Ala His Gln Gly His Gln Leu Ser Thr Leu Asp Glu Ala 230 235 240	838
ttt gaa gaa tta aga agc aaa gac tca ggt gga ctg aag gcc gct atg Phe Glu Glu Leu Arg Ser Lys Asp Ser Gly Gly Leu Lys Ala Ala Met 245 250 255	886
atc gaa ttg gtg gaa agg ttg aag ttc aag agc tca gac cct aaa gta Ile Glu Leu Val Glu Arg Leu Lys Phe Lys Ser Ser Asp Pro Lys Val 260 265 270	934
act cgg gac caa atg aag atg ttt ata cag cag gaa ttt aag aaa gtt Thr Arg Asp Gln Met Lys Met Phe Ile Gln Gln Glu Phe Lys Lys Val 275 280 285	982
cag aaa gtg att gct gat gag gag cag aag gcc ctt cat cta gtg gac Gln Lys Val Ile Ala Asp Glu Glu Gln Lys Ala Leu His Leu Val Asp 290 295 300 305	1030
atc caa gag gca atg gcc aca gct cat gtg act gag ata ctg gca gac Ile Gln Glu Ala Met Ala Thr His Val Thr Glu Ile Leu Ala Asp 310 315 320	1078
atc caa tcc cac atg gat agg ttg atg act cag atg gcc caa gcc aag Ile Gln Ser His Met Asp Arg Leu Met Thr Gln Met Ala Gln Ala Lys 325 330 335	1126
gaa caa ctt gat acc tct aat gaa tca gct gag cca aag gca gag ggc Glu Gln Leu Asp Thr Ser Asn Glu Ser Ala Glu Pro Lys Ala Glu Gly 340 345 350	1174
gat gag gaa gga ccc agt ggt gcc agt gaa gaa gag gac aca tgaaggctt Asp Glu Glu Gly Pro Ser Gly Ala Ser Glu Glu Glu Asp Thr	1225

355

360

1241.22
365

gctaccccc	gtggaaaatc	atccccctccc	cttgtgtgta	tgtgacagcg	tgtatgtaac	1285
ggcttctgat	ttctgtgaaa	gctgtctcagc	aacaaacgta	cttccaccag	atgtgtcccc	1345
agatccacag	caggcacata	tctctccaag	ggatgaccag	ttttatgctt	actgtgtgct	1405
tctcatcccc	tggttgtggt	aggtcaagga	aaagagcccc	tttgatccac	caggagcaat	1465
taagaaagg	ccttcaggta	atccctcaat	ggctgctttg	aacttactca	ggaaagccag	1525
cccccataat	attgtattac	caaacagtat	cgctttgtta	ggaaggatct	ggaataatct	1585
tgaagggaag	tcagagtttt	ctccctgcct	attaacaaaa	acccaatttt	gttcatattg	1645
aagcatgaaa	taaatgagag	caaggtaggg	ccaaattaac	tcttgtggac	agtcacctaaa	1705
agtccagttc	tacatttgtg	aaaattgtgg	tgccatgaat	taagatggat	gactggaaaa	1765
aggtgttgga	gaaagagtta	aagatgagga	agagatat	ttagtatatg	aagttatcca	1825
ggacttgata	ttcataattc	agtgtgtg	aaatgaaaaa	aatgattgaa	gaggtggaac	1885
ggaaatgacc	ttagggggaa	aaaaaaggac	caaagaagtc	tgattaaaag	ttgaaatcag	1945
tatttctgaa	ttcaaattgc	ttgaatttcc	aaaatagtca	gtaaaggatc	taatagaacc	2005
agaattat	gggtgaattc	tgcaggtttt	atgggcttgt	cacaacgtga	agggctggaa	2065
tgtatattac	caaattgggaa	tttccattgt	aggtttttgc	tagtcccacc	cccatatttag	2125
cctaatttgg	cttaaacgca	gtatggggag	aattgttccc	attccatgtg	ttctgaattc	2185
agctcatctc	ccagcatata	gatataatcct	cctttaactc	cgaccagaac	ccttcttcct	2245
gtggcactcc	ccaccatag	accttcagat	catctcccac	accctggatc	tcactctcct	2305
cttagtaaca	gagacactcc	tgagggttga	cttccttgc	tttctctact	tccaaatcac	2365
aatttcttac	aaccaagctt	tgtgtctccg	agtaagcagg	gatgtactag	gggaatgtaa	2425
aactgcaaac	ttaaaaaacct	gcatcttctt	gaagcatcag	ttttacttac	caaattggtt	2485
agagtcataa	gatgacctat	ttttatataa	aagttatatt	atagaataaa	atgttcatac	2545
gcatagactg	ttaag					2560

<210> 173

<211> 367

<212> PRT

<213> Homo sapiens

<400> 173

Met	Arg	Pro	Arg	Gly	Arg	Lys	Ala	Ala	Ser	Pro	Gly	Ala	Pro	Arg	Pro
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Trp	Pro	Arg	His	Ser	Thr	His	Met	Ala	Ser	Gly	Val	Gly	Ala	Ala	Phe
			20					25					30		
Glu	Glu	Leu	Pro	His	Asp	Gly	Thr	Cys	Asp	Glu	Cys	Glu	Pro	Asp	Glu
		35					40					45			
Ala	Pro	Gly	Ala	Glu	Glu	Val	Cys	Arg	Glu	Cys	Gly	Phe	Cys	Tyr	Cys
	50					55					60				
Arg	Arg	His	Ala	Glu	Ala	His	Arg	Gln	Lys	Phe	Leu	Ser	His	His	Leu
	65				70					75					80
Ala	Glu	Tyr	Val	His	Gly	Ser	Gln	Ala	Trp	Thr	Pro	Pro	Ala	Asp	Gly
			85					90						95	
Glu	Gly	Ala	Gly	Lys	Glu	Glu	Ala	Glu	Val	Lys	Val	Glu	Gln	Glu	Arg
	100							105					110		
Glu	Ile	Glu	Ser	Glu	Ala	Gly	Glu	Ser	Glu	Ser	Glu	Glu	Glu	Ser	
	115						120					125			
Glu	Ser	Glu	Glu	Glu	Ser	Glu	Thr	Glu	Glu	Glu	Ser	Glu	Asp	Glu	Ser
	130					135					140				
Asp	Glu	Glu	Ser	Glu	Glu	Asp	Ser	Glu	Glu	Glu	Met	Glu	Asp	Glu	Gln
	145					150				155					160
Glu	Ser	Glu	Ala	Glu	Glu	Asp	Asn	Gln	Glu	Gly	Glu	Ser	Glu	Ala	
			165					170					175		
Glu	Gly	Glu	Thr	Glu	Ala	Glu	Ser	Glu	Phe	Asp	Pro	Glu	Ile	Glu	Met
			180					185					190		
Glu	Ala	Glu	Arg	Val	Ala	Lys	Arg	Lys	Cys	Pro	Asp	His	Gly	Leu	Asp
	195						200					205			
Leu	Ser	Thr	Tyr	Cys	Gln	Glu	Asp	Arg	Gln	Leu	Ile	Cys	Val	Leu	Cys
	210					215					220				
Pro	Val	Ile	Gly	Ala	His	Gln	Gly	His	Gln	Leu	Ser	Thr	Leu	Asp	Glu
	225				230					235					240
Ala	Phe	Glu	Glu	Leu	Arg	Ser	Lys	Asp	Ser	Gly	Gly	Leu	Lys	Ala	Ala

1241.22

<400> 178
ggaaagctct ccgtggctaa caag 24

<210> 179
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of the artificial sequence:a synthetic DNA

<400> 179
catagtcctt gacaagggtc acag 24

<210> 180
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of the artificial sequence:a synthetic DNA

<400> 180
cccatcacca tcttccagga gc 22

<210> 181
<211> 26
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of the artificial sequence:a synthetic DNA

<400> 181
ttcaccacct tcttgatgtc atcata 26